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A;Title: The primary structure of a human IgG2 heavy chain: geneti A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'z',59,'A',61-193,'D',195-325 <WAN>
A;Residues: 1-19,'Q',21-57,'z',59,'A',61-193,'D',195-325 <WAN>
A;Rolecule type: protein
A;Rolecule type: protein
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constar
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-1:
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: Arrec on the amino acid sequence
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C;Comment: The heavy chain disease protein Wis is shown.
C;Gennetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 11432.33-14432.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMN:
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;203-270/Domain: immunoglobulin carboxylic acid (Gln) #status experimental
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A;Accession: A93906
A;Molecule type: DNA
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A;Residues: 1-326 <ELL>
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-2 chain C region - human C;Speciles: Homo sapiens (man) C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000 C;Accession: A93906; A92809; A90752; A93132; A02148 R;Ellison, J; Hood, L. Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
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G2HU
A;Title: A note on the amino A;Reference number: A93132; M A;Contents Zie A;Contents Zie A;Accession: A93132 A;Molecule type: protein
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Best Local Similarity
Matches 209; Conserv
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PMID:118920
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A;Title: Nucleotide sequence o: A;Reference number: A90933; MU A;Accession: A99933 A;Molecule type: DNA A;Residues: 1-327 «ELL» A;Residues: 1-327 «ELL» A;Residues: 1-327 «ELL» A;Residues: 1-327 «ELL»

determined from S.H.; De Vries,

from the germline gene ries, G.M.; Milstein, C.

R;Ellison, J.; Buxbaum, DNA 1, 11-18, 1981

J.; Hood,

e of a human immunoglobulin MUID:83157104; PMID:6299662

C-gamma4

Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #sequence revision C;Accession: A99933; A90249; A02150

02-Apr-1982

#text_change 16-Jul-1999

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A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-8s/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;133-202/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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A;Cross-references:
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R; Hofmann, T.; Parr,
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                                                                                                                    LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
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MHEALHNHYTQKSLSLSPG
                                             MHEALHNHYTOKSLSLSPG
                                                                                                                                                                                     VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC
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Pred. No. 7.5e.
12; Mismatches
  325
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7.5e-62;
les 12;
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in having
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60-Ala and in the
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N;Alternate names: T-cell surface antigen T4/Leu 3
(;Speciles: Homo sapiens (man)
(;Speciles: Homo sapiens (man)
(;Speciles: Homo sapiens (man)
(;Date: 28-May-1986 #sequence revision 31-Dec-1988 #text_change 20-Apr-2001
(;Accession: A90872; A32722; A34194; A55287; I54176; I54297; A02109; A30039
(;Accession: A90872; A32722; A34194; A55287; I54176; I54297; A02109; A30039
(;Accession: A90872; A32722; A34194; A55287; I54176; I54297; A02109; A30039
(;Accession: A90872; A32722; A34194; A55287; I54176; I54297; A02109; A30039
(;Accession: Apolitical Company of Association (A) Application (A)
                                                                              Cell 55, 541, 1988
A;Title: Corrected CD4 sequence.
A;Reference number: A90907; MUID:89028665; PMID:3263213
A;Contents: annotation; revision to residue 26
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The isolation and nucleotide sequence of a cDNA encoding the T cell A;Reference number: A90872; MUID:85254948; PMID:2990730 A;Accession: A90872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWHUT4
T-cell surface glycoprotein CD4 precursor [validated] - human
N-Alternate names: T-cell surface antigen T4/Leu 3
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201.247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Map position: 14932.33-14932.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
F;99-110/Region: hinge
                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Regidueg: 1-25, 'N', 27-458 < MAD>
A; Experimental source: clone pT4B
R; Littman, D.R., Maddon, P.J.; Axo
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A; Title: Human immunoglobulin sublclasses.
A; Reference number: A90249; MUID:70207560;
A; Title: A CD4 domain important for HIV-mediated syncytium A; Reference number: A32722; MUID:90182664; PMID:2107024
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A; Residues: 1-30;81-326 <PIN>
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P.J.; Axel,
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Pred. No. 3.8e-61;
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein f;1-25/Domain: signal sequence #status predicted <SIG> F;26-458/Porduct: T-cell surface glycoprotein CD4 #status experimental <MAT> F;34-111/Domain: immunoglobulin homology <IM1> F;34-111/Domain: immunoglobulin homology <IM1> F;136-186/Domain: immunoglobulin homology <IM3> F;216-299/Domain: immunoglobulin homology <IM3> F;321-372/Domain: immunoglobulin homology <IM3> F;321-372/Domain: transmembrane #status predicted <INT> F;397-420/Domain: transmembrane #status predicted <INT> F;421-458/Domain: intracellular #status predicted <INT> F;41-109.155-184,328-370/Disulfide bonds: #status experimental F;296,325/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 26-426, 428-458 <CAM>
A;Residues: 26-426, 428-458 <CAM>
R;Carr, S.A.; Hemling, M.E.; Folena-Wasserman, G.; Sweet, R.W.; Anumula, K.; Barr, J.
J. Biol. Chem. 264, 21286-21295, 1999
J. Biol. Chem. 264, 21286-21295, 1999
A;Title: Protein and carbohydrate structural analysis of a recombinant soluble CD4 x
A;Reference number: A34194; MUID:90078232; PMID:2592374
A;Concepts: disulfide bonds; carbohydrate-binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:U47924; GB:M86525; GB:U72506; NID:g1633547; PIDN:AAB51309.1; PID:gR;HOdge, T.W.; Sasso, D.R.; McDougal, J.S.
Hum. Immunol. 30, 99-104, 1991
A;Title: Humans with OKT4-epitope deficiency have a single nucleotide base change in the A;Reference number: I54297; MUID:91216786; PMID:1708753
A;Accession: I54297
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A;Residues: 26-394 <CAR>
R;Lederman, S.; DeMartino, J.A.; Daugherty, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 14, 590-597, 1992
A;Title: A human dimorphism resulting from loss of an Alu.
A;Reference number: I54176; MUID:93052387; PMID:1330888
A;Accession: I54176
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A;Title: A single amino acid substitution in a common African allele of the CD4 molecule A;Reference number: A53287; MUID:92072595; PMID:1961196

A;Accession: A53287
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A;Residues: 1-264,'w',266-458 <RE2>
A;Residues: 1-264,'w',266-458 <RE2>
C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine
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A; Residues: 1-72 < RES>
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                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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      61
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                            MRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
      ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                    Conservative
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from NCBI backbone (NCBIP:68249)
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Pred. No. 3.9e
0; Mismatches
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Ig gamma-3 chain C region, membrane-bound form - mouse (,Species: Mus musculus (house mouse) C;Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: A02156; A02155 R;Mels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, EMBO J. 3, 2041-2046, 1984 A;Reference number: A02156; MUID:85027161; PMID:6092053 A;Accession: A02156; MUID:85027161; PMID:6092053
                                            G1MSM
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F;136-205/Domain: immunoglobulin homology <IM2>
F;242-309/Domain: immunoglobulin homology <IM3>
F;346-352/Domain: transmembrane #status predicted <TWM>
F;363-398/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la G:Superfamily: immunoglobulin C region; immunoglobulin homology cyKeywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; 193/Domain: immunoglobulin homology cyMi>
    Ig gamma-1 chain C region, membrane-b
C; Species: Mus musculus (house mouse)
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A;Residues: 328-332,'G',334-341,'Q',343-387,'F',389-398 <KOM>
A;Cross-references: GB:K00688
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NTITLE: The structure of the mouse immunoglobulin in gamma-3 membrane graph A;Reference number: A02155; MUID:84041483; PMID:6314258
A;Accession: A02155
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A; Residues: 1-398 <WEL>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                         SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                            QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVSQLELQDSGTW----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP--EL
                                                                                                                                                                                                                   REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPFILDSDGTYFLYSKLTVDT
                                                                                                                                                                                                                                                                                                      QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
                                                                                                                                                                                                                                                                                                                                                                                        LGGPSVFIPPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
                                                                                                                                                                                                                                                                                                                                                                                                                 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCPPGNI
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                                                                                                                                   DSWLQGEIFTCSVVHEALHNHHTQKNLSRSPELELNETCAEAQDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.6%;
                          membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
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Pred. No. 4.3
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Ig heavy chain precursor (B/MT.4A.17.H5.A5) - N;Alternate names: Ig gamma-1 chain C region C;Species: Bos primigenius taurus (cattle)
                                                                     S22080
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A;Note: the sequence was determined from the germline gene R;Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Be Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
A;Title: mRNA for surface immunoglobulin gamma chains encodes A;Reference number: A02160; MUID:82197626; PMID:6804950
A;Accession: A02160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k C;Complex: An immunoglobulin heterotetramer subunit and IgM, the subunits associate into hain disulfide bonds. In some cases; inch as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology c;Keywords: immunoglob
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A;Residues: 323-393 <TYL>
A;Residues: 323-393 <TYL>
R;Rogers, J; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl,
Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini
A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Recession: B02158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;340-357/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 323-366 < ROG>
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A; Residues: 1-393 < HON>
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Best Local S
Matches 177
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431
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                                                                                                                                                                                                                                                                                      KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
        GLQLDETCAEAQDGELDGLWTT
                                                                                                                                                       QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                ISKODPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS
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                                                                             QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
                                                                                                                                                                                                                                         AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG
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intracellular #status predicted <INT>
site: carbohydrate (Asn) (covalent) #status
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Pred. No. 1.1e-49;
0; Mismatches 60;
452
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RESULT 14
G2MSAM
Ig gamma-2a chain C region, membrane-bound form - C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 31-Mar-1991
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin
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A; Residues: 1-470 < SAN.
A; Residues: 1-470 < SAN.
A; Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1;
A; Cymons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region A; Reference number: S06610; MUID:90097956; PMID:2513487
A; Accession: S06610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: $22080
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Best Local :
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                                                                                                                                                                                                                                            AVEWESNGOP--ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 420
                                                                                                                                                                                                                                                                                     EFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPPQEELSKSTVSLTCMVTSFYPDYI
                                                                                                                                                                                                                                                                                                      EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
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                                                                                                                                                                                                                                                                                                                                                                                  EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                    AHPASSTKVDKAVD----PTCKPSPCD---CCPPPELPGGPSVFIFPPKPKDTLTISGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRTP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGCLVSSYMPEPVTVTWNSGALKSGVHTFPAVLQSSGLYSLSSMVTVPGSTSGQTFTCNV
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                                                                                                                                   YTOKSTSKSAG
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llarity 43.6%;
Conservative 52
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 31-Mar-1991 #text_change 16-Jul-1999
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Ig gamma 2a chain constant region - pig (f C;Species: Sus scrofa domestica (domestic C;Date: 21-Feb-1997 #sequence_revision 21-C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;137-206/Domain: immunogropurm numbers; 7:206/Domain: transmembrane #status predicted <TMM>F;346-363/Domain: intracellular #status predicted <INT>F;364-399/Domain: intracellular #status predicted <INT>F;180/Binding site: carbohydrate (Asn) (covalent) #status
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A;Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
A;Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp capped) in the subunits associate into late hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into late hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into late hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into late hain display.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; jumunoglobulin homology
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C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspond C;Comment: Cell lines producing IGG contain two mRNA species for Ig gamma chains. The marhat it contains an alternative 3' end, encoded in separate exons, that is homologous with C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence was determined from the germline gene R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: B32657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Immunol. 26, 819-826, 1989
A;Title: Sequence and polyademylation site determination of the murine immunoglobulin A;Reference number: 157809; MUID:90097953; PMID:2513486
A;Accession: 157809
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A; Residues: 1-329, 'K' <YA2>
R; Hall, B: Milcarek, C.
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A; Residues: 373-399 < RES>
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A; Residues: 329-399 < YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: alternative splicing; duplication; glycoprotein; 137-206/Domain: immunoglobulin homology <IMM>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      VFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                               SYSCSVVHEGLHNHHTTKSFSRTPGLDLDDVCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFPPKIKDVLMISLSPIVICVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERN
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Pred. No. 4.2e-48;
4; Mismatches 60;
                                                                                                                                                                    pig (fragment)
                                                                                                        tic pig)
21-Feb-1997
                                                                                                     #text_change
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A;Molecule type: protein
A;Residues: 1-47,'E','49-71,'PV',72-128 <PRA>
A;Residues: C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-323 < LERA
A; Residues: 1-323 < LERA
A; Note: this sequence has the dl2 allotypic marker, 104-
R; Pratt, D.M.; Mole, L.E.
Blochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the
A; Reference number: A90290; MUID: 76135469; PMID: 1243651
A; Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma chain C region - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999 C;Accession: A91749; A90290; A93928; A90245; A94416; A02161 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinar A;Reference number: A91749; MUID:84030930; PMID:6313520 A;Accession: A91749
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GHRB
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C;Superf
A; Molecule type: mRNA
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Cross-references: GB: M16426; NID: g165111; PIDN: AAA31289.1; PID: g165112
A; Note: this sequence has the d11 allotypic marker, 104-Met, and the e15
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-328 <KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVTCVVVDVSQENPEVQPSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
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58.5%;
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1. No. 7.2e-48;
-hes 57;
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밁

19

-SSKSYTCNV--NHPATTTKVDKRVGTKTKPPCP-

ICPACE

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Ig gamma 4 chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 C;Accession: I47162 #sequence_revision 21-Feb-1997 R;Kacskovics, I.; Sun, J.; Butler, J.E. J. Immunol: 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
147162
                                                                                                                                                                                                                                                                                   R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine
A;Reference number: I47158; MUID:95015845;
A;Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 129-131:155-172,'D',174-184,'A',186,'E',188-200,'D',202-2:
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two idhain disulfide bonds. In some cases, such as IQA and IGM, the subunitt
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Reywords: immunoglobulin homology CIMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 132-143,'E',145-161 <FRU>
R;HHI1, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; I
in Gamma Globulins, Nobel Symp. 3, Killander, J.,
A;Reference number: A94416
A;Accession: A94416
á
                                                                                                                         A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                        A;Cross-references: EMBL:U03782; NID:g433129;
                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-277 < KA
                                                                                                                                                                                                                                                                A; Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence studies of the Fd section of the heavy chain A;Reference number: A90245; MUID:70110015; PMID:5461106 A;Accession: A90245 A;Molecule type: protein
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Matches
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les 178; Conserv
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ilarity 61.0%;
Conservative 3
                                             Conservative
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                                                                                                                                                                                                                                                                    translated
                                                            37.2%;
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                                           Score 898; DB 2
Pred. No. 9e-48;
3; Mismatches
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Pred. No. 9.4e-48;
4; Mismatches 64
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                                                                                                                                                                                                                                                                    GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                          IgG identified PMID:7930579
                                                                                                                                                                                                          PIDN:AAA52220.1; PID:g433130
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                                                                                   2;
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                                                43;
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                                                                                 Length
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Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 16-Jul-1999
C;Accession: A94553; A90352; Ā90359; A90384; A90385; A02I51
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
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F;133-202/Domain:
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: 147158; MUID:95015845; PMID:793
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: 147160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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A; Reference number: A; Accession: A94553
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|||||:||:|||||||||:||:||
SPGPSVF1FPPKPKDT1M1SRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEE
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                                                                                                                                                                                                                    DKASWOGGGI FOCAVMHEALHNHYTOKS I SKTPG
                                                                                                                                                                                                                                                                                        AEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSV
                                                                                                                                                                                                                                                                                                              RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                             OFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALFAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPGPSAPIFPPXPXDTLMISRTPKVTCVVVDVSQENPEVQPSWYVDGVEVHTAQTRPXEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: U03780; NID: g433125; PIDN: AAA52218.1; PID: g433126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.2%;
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Pred. No. 1.1e-47;
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A; Residues: 1-3 </
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Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy
A;Reference number: A90359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 4-68 < BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A90359
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                                                                                        SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLT 396
                                                                                                                                                             EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
                                                                                                                                                                                                                                     LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                                                                      LOSGLYSLTSMVTVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPCTCPK---CPPPE
                                                                     SRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLT
                                                                                                                                           EQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPP
                                                                                                                                                                                                                                                                                                                          IQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTC--PE
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                                                                                                                                                                                                                                                                                                                                                        Score 894.5; DB 1;
Pred. No. 1.8e-47;
Mismatches 60;
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Indels Length

9,

Gaps

4

114

234

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A; Molecule type: protein
A;Residues: 227-311 <TR2>
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Fitle: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Fitle: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Fitle: Interchain disulfide bridges
A;Fitle: Interchain disulfide bridges
A;Fitle: Interchain disulfide bridges
A;Fotle: Cys-105; Asia in MuID:71058474; PMID:4922544
A;Contents: annoctation; disulfide bonds
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaps dain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;131-204/Domain: immunoglobulin homology <IM1>
F;28-79/Disulfide bonds: #status experimental
F;143-07/Disulfide bonds: #status experimental
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A;Residues: 69-133;312-329 <TUR>
R;Tracey, D.B.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Fitle: Primary structure of the C-H2 homology region 1
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Residues: 134-226 <TRA>
Biochemistry 13, 4804-4811, 1974
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
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Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
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#status experimental
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C;Genetics:
A;Gene: IgG1
C;Superfamily: immu
F;133-202/Domain: 1
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A;Title: Five putative subclasses of swine A;Reference number: I47158; MUID:95015845; A;Acetesion: I47158
A; Molecule type: DNA
A; Residues: 335-378 < ROG>
A; Note: the translation o
                                                       A.Cross-references: GB:J00462
R;Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: A02158
                                                                                                                                                                                                        R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding
A;Reference number: A02154; MUID:82222190; PMID:6283537
A;Accession: C02154
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G2MSBM
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
                                                                                                                                                                                                                                                                                                          Ig gamma-2b chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Date: 17-Dec-1922 #sequence revision 31-Mar-1991 #text_change C;Accession: C02154; A02158; B02157
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A; Residues: 335-405 < YAM>
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A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1;
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Best Local Similarity
Matches 180; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVEFKIDI-VPCPAPEPKS--CDKTH------TCPELLG----GPSVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKFECAVMHEALHNHYTQKSISKTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V$VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGIHQPQTCPICPGCEVAGPSVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDGTFFLYSKLAVDKARWDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQFNSTYRV
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immunoglobulin homology <IMM>
     of the
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     first
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     exon
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     of the
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     membrane-bound
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A;Cross-references: GB:M31135
R;Fomsgaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules:
A;Reference number: A46534, MUID:93049640; PMID:1425921
A;Accession: A46534
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual
                                                                                                                                                                                                                           Cell 60, 747-754, 1990
A;Title: A CD4 domain important for HIV-mediated syncytium formation A;Reference number: A32722; MUID:90182664; PMID:2107024
A;Accession: B32722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IQA and IGM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;143-212/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-335,'K' <YA2>
G;Comment: The sequence of residues 1-334 was assumed to be identical with the correspon-
C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-432 < CAM>
                                                                                                                                                                                                                                                                                                                      C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
                                                                                                                                                                                                                                                                                                                                                                                                T-cell surface glycoprotein CD4 - chimpanzee
N,Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Pan troglodytes (chimpanzee)
C;Date: 30-Sep_1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell surface glycoprotein CD4 -
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A; Accession: B02157
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A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain A;Reference number: A02157; MUID:80120716; PMID:6766534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCNVRHEGLKNYYLKKTISRSPGLDLDDICAEAKDGELDGLWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEKEKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
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A;Residues: 3-399 <FOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
C;Comment: This protein is expressed on most thymocytes, on a subset of mature T-ce C;Comment: This protein is expressed on most thymocytes, on a subset of mature T-ce C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein C;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-371/Domain: extracellular #status predicted <EXT>
F;9-86/Domain: immunoglobulin homology <IM1>
F;111-161/Domain: immunoglobulin homology *IM1>
F;191-274/Domain: immunoglobulin homology <IM3>
F;296-347/Domain: immunoglobulin homology <IM4>
F;395-347/Domain: immunoglobulin homology <IM4>
F;372-395/Domain: immunoglobulin homology <IM4>
F;372-395/Domain: intracellular #status predicted <INT>
F;36-843/Domain: intracellular #status predicted <INT>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma 3 chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 C;Accession: I47161 R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG iden A;Reference number: I47158; MUID:95015845; PMID:793 A;Accession: I47161
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A; Residues: 1-328 < KAC>
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Best Local
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Best Local :
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                             EFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTVTCLVIGFYPPDI
                                                                                                                                                                                      PATTTKVDKRVGTKTKPPCP-----ICPGCEVAGPSVF1FPPKPKDTLMISQTP
                                                                                                                                                                                                               KKVEFKID------IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPKFKDTLMISRTP
                                                                                                                                                                                                                                                                   EPVTMTWNSGALTSGVHTFPSV--LQPSGLYSLSSMVTVPASSL---SSKSYTCNV--NH
                                                                                                                                                                                                                                                                                                        QSLTLT----LESPPGSSPSVQCRSPRG-KNIQGGKTLSVSQLELQDSGTWTCTVLQNQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDQGNFTLIIKNLKIEDSDTYICEVGDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                             36.2%; Score 873; DB 2; 57.6%; Pred. No. 3.7e-46; ative 37; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 3.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                 61;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 328;
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monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S:; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porph A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-329 <WEL>
A; Cross-references: GB: J00451
A; Note: the sequence was dete
C; Genetics:
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C;Complex: An immunoglobulin
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Ig gamma-3 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: B02156 R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, EMBO J. 3, 2041-2046, 1984 A;Pitle: Structure analysis of the murine IgG3 constant region gene. A;Reference number: A02156; MUID:85027161; PMID:6092053 A;Accession: B02156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul C;KeyB)Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;136-205/Domain: immunoglobulin homology <IM2>
F;242-309/Domain: immunoglobulin homology <IM3>
F;179,322/Binding site: carbohydrate (Asn) (covalent)
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                               QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP 236
                                                                                                                                                                                                                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                    LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCPPGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSQLELQDSGTW----TCTVLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCP--EL
                                                                                                                       REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 857.5; DB 1;
Pred. No. 3.2e-45;
B; Mismatches 57;
                                                           431
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A; Molecule type: mRNA
A; Residues: 1-472 < PAT>
A; Residues: 1-472 < PAT>
A; Cross-references: EMBL: X69797
C; Superfamily: immunoglobulin C region; immunoglobulin
C; Keywords: immunoglobulin
F; 277-346/Domain: immunoglobulin homology < TMM-
                                                                                                                                                                                                                                                                                     Ig gamma-1 chain - sheep (fragment)
(;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
(;Accession: S31459
R;Patri, S:; Nau, F:
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Status: preliminary
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C;Comment: This catalytic antibody has peroxidase oxidase activity. C;Comment: This catalytic antibody has peroxidase oxidase activity. C;Superfamily: immunoglobulin C region; immunoglobulin homology F;251-320/Domain: immunoglobulin homology <IMMS
F;22/Disulfide bonds: interchain (to 98) #status predicted F;99/Disulfide bonds: interchain (to 109) #status predicted
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Best Local S
Matches 196
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Best Local S
Matches 188
                                                                                                                                                                                          -346/Domain: immunoglobulin homology <IMM>
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                                                               TLSVTCTISGFSLNNYGVDWVRQAPGKALEWLGGSGYDEDIDYNPVLKSRLSITKDTSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
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                              LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE-----VQLLVFGLTANSDTHL
                                                                                              TVELTCTAS -- QKKSIQFHWKN--- SNQIKILGNQG--SFLTKGP---SKLNDRADSRRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP
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 ----QVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWGPGLLISVLSAST----
                                                                                                                               Conservative
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                                                                                                                                             35.4%; Score 854.5; DB 2; 42.2%; Pred. No. 7.5e-45;
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Pred. No. 6.9e-45;
                                                                                                                              Mismatcheв 119;
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209

329

REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 388 VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV 365 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP KC----PAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE SCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE

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Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, Febru
A;Reference number: S37483
A;Accession: S37483
A;Accession: S37483
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin C;Keywords: immunoglobulin Homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-469 < DUC>
                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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193
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                              -SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPK 208
                                                                          TTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTF
                                                                                                               LTLTLESPPGSSPSVQ----CRSPRGKNIQGG--
                                                                                                                                                                                          RSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQS 138
                                                                                                                                                                                                                                                                       LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
PAVLOSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---PC
                                                                                                                                                       ATLTVDTSSSTAYMQLSSLTSEDTAVYFC
                                                                                                                                                                                                                                  LVKPGASVKISCKASGYTFTDYY---INWVKQKPGQGLKWIGWIYPASGNTKYNENFKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTHTC--PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                              35.2%;
                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                Score 850.5; DB 2;
Pred. No. 1.3e-44;
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                                                                                                                                                                                                                                                                                                             Mismatches 125;
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C; Keyworu.
F;113-182/Domain:
A; Molecule type: DNA
A: Residues: 227-333 <BR2>
                                      A;Molecule type: DNA
A;Residues: 1-33 <BRU>
A;Residues: 1-33 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold,
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Status: preliminary
                                                                                                                                                                                                                                                                 Ig gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
R;Brueggemann, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Isolation and sequence of sheep Ig H and L chain cDNA A,Reference number: A30554; MUID:89093962; PMID:2492052 A,Accession: C30554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: C30554
R;Foley, R.C.; Beh, K.J.
J. Immunol. 142, 708-711, 1989
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                                                                                                                                                                                                             Gene 74, 473-482, 1988
A;Title: Evolution of the r
A;Reference number: PS0017;
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C30554
Ig heavy chain C region
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Species: Ovis orientalis aries, Ovis amm
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Best Local Similarity
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60.7%;
                                                                                                                                                                                                               rat immunoglobulin gamma heavy-chain 7; MUID:89232738; PMID:3149946
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Pred. No. 4.6e-44;
7; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431
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Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 96/1; 117/1; 227/1 c;Superfamily: immunoglobulin C;Keywords: immunoglobulin F;20-82/Domain: immunoglobulir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;231-340/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 12
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-446 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S40295
                                                                                                                                                                                                                                                                                                     7;231-340/Domain: C2 region <CH2>
7;341-446/Domain: C3 region <CH3>
7;341-446/Domain: C3 region <CH3>
7;340-427/Domain: immunoglobulin homology <IMM>
7;340-427/Domain: immunoglobulin homology <IMM>
7;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
7;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
7;22-96,144-199,261-321,367-425/Disulfide bonds: predicted
7;224,227,229/Disulfide bonds: interchain #status predicted
7;227,219/Disulfide bonds: interchain #status predicted
7;227,219/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Keywords: immunoglobulin;20-82/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;1-446/Product: Ig gamma-2a chain #status
;1-117/Domain: V-D-J region <VDJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: disulfide bond; glycoprotein;
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRAPFVCSVVHEGLHNHHVEKSISRPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQPREEQYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
GKATLTVDTSSSTAYMQLSSLTSEDSAVYFC-
                                           SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                                                                                                 LVRPGASVKISCKASGYTFTDYYIHW
                                                                                                                                                  LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPQVYVMGPPTEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTW----TCTVLQ--NQKKVEFKIDI-----VPCPAPEPKSCDKTHTC--PELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLNVERSRWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.5%;
                                                                                                                                                                                                                                 34.2%;
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                                                                                                                                                                                                   Score 825; DB 2;
Pred. No. 4.4e-43;
0; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 833; DB 2
Pred. No. 1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332
                                                                                                 VKQRPGEGLEWIGWIYPGSGNTKYNEKFK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                      Length 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyroglutamic
ARGGKFAMDYWG
                                                                                                                                                                                                      92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
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108
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A;Introns: 98/1; 113/1; 220/1
C;Superfamily: immunoglobulin C region; immuno
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-326 <BRUs
A;Residues: 1-326 <BRUs
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: C25941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
PS0017

Ig gamma-1 chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990
C;Accession: PS0017; C25941
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A:Molecule type: DNA
A:Residues: 220-326 <BR2>
C:Genetics:
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Gene 74, 473-482, 1988
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Best Local Similarity
Matches 163; Conserv
                346
                                                 180
                                                                                   286
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                                                                                                                                                           226
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                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                28
                                                                                                                  QTVTCNVAHPASSTKVDKKI-----VPRNC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSD
              NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                RSVSELPILHODWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPTKEEMTQ
                                                                                                                                                                                                                             ---TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG------PSV
                                                                                                                                                                                                                                                                LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LQSGLYTLTSSVTV-PSSTWPS
                                                                                                                                                                                                                                                                                                  LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSYFMYSKLRVEKKOWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGTSVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSLTLTLESPPGSSPSVQ-----CRSPRGKNIQGG-----KTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                   34.1%; Score 823.5; DB 2; 50.0%; Pred. No. 3.8e-43; tive 53; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change
                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
                                                                                                                                                                                          GGDCKPCICTGSEVSSV
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                   345
                                                                                                                      179
                                                                                                                                                       285
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                                                                                                                                                                                          119
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                                                239
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                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiboo
Gene 9, 87-97, 1980
A;Title: Immunoglobulin gamma-1 heavy chain gene: structural
A;Reference number: A26234; MUID:80202559; PMID:6769752
A;Contents: MOPC 31C
A;Accession: A26234
                                                                             A;Cross-references: GB:J00453
A;Note: the sequence was determined from the germline A;Note: Lys-324 is removed posttranslationally R;Obata, M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kata Gene 9, 87-97, 1980
                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 24-Sep-1981 #text_change 16-Jul-1999
C;Accession: A02159; A26234; A26236
R;Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahash Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gammal A;Reference number: A02159; MUID:80045036; PMID:115593
                                                                                                                                                                      A;Accession: A02159
A;Molecule type: DNA
A;Residues: 1-324 <HON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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Best Local
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Y.; Kataoka, T.; Kawakami, T.; Takahashi,

chain

ω

N.; Kataoka,

: : gene

Shimizu,

Α.,

¥.; Í'n

cloned Mano,

ø Se gene

mouse

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A;Cross-references: EMBL:X07189; NID:g57602; PIDN:CAA30169.1; PID:g663228 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,Brueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, Bur. J. Immunol. 18, 317-319, 1988
A,Title: Sequence of a rat immunoglobulin gamma-2c heavy chain A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847
A;Residues: 1-329 < BRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2c chain C region - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 01-Dec-1989 #sequence_revision 01-D C;Accession: $00847
                                                                                                                                                         NVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                            DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
HEALHNHHTQKNLSRSPG
                                      HEALHNHYTOKSLSLSPG 431
                                                                             VTSFYPASISVEWERNGELEQDYKNTLPVLDSDESYFLYSKLSVDTDSWMRGDIYTCSVV
                                                                                                                                                                                                                                  VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                    SSTWSSOTVTCSVAHPATKSNLIKRIEP-RRPKPRPPTDICSCDDNLGRPSVFIFPPKPK
                                                                                                                                                                                                                                                                                                                                                      SGTW-----TCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK 233
                                                                                                                                                                                                                                                                                                                                                                                                               34.1%;
                                                                                                                                                                                                                                                                                                                                                                                               45;
    328
                                                                                                                                                                                                                                                                                                                                                                                                               Score 823; DB 2;
Pred. No. 4.1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-Dec-1989
                                                                                                                                                                                                                                                                                                                                                                                                 56;
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                               6;
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                                                                                                                      413
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ext

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Ig gamma-Zb chain - mouse

Gyspecies: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Becies: Mus-1980 #sequence revision 01-Dec-2000 #text change 01-Dec-2000

C;Accession: S25057; A02157; A26235; A26232; A26233; A53598

C;Accession: S25057; A02157; A26235; A26232; A26233; A53598

R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaldeuberted to the EMBL Data Library, July 1992

submitted to the EMBL Data Library, July 1992

* Precription: Production of a Tobacco mosaic virus (TMV) inactivating neot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nimmunoglobulin heterotetramer subunit consists of two identical light (kapperson disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin P;20-84/Domain: immunoglobulin homology <IM1>
F;98-110/Region: hinge
F;131-200/Normain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Rogers, J.; Clarke, P.; Salser, W.
Nucleic Acids Res. 6, 3305-3321, 1979
A;Title: Sequence analysis of cloned cDNA encoding part A;Reference number: A26236; MUID:80012837; PMID:113776
A;Contents: MOPC 21
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F;237-304/Domain: immunoglobulin homology <IM3>
F;237-304/Domain: immunoglobulin homology <IM3>
F;27-82,138-198,244-302/Disulfide bonds: #status experimental
F;102/Disulfide bonds: interchain (to light chain) #status experimental
F;104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;174/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Adecugbo, K.

J. Biol. Chem. 253, 6068-6075, 1978

J. Biol. Chem. 253, 6068-6075, 1978

A;Title: Evolution of immunoglobulin subclasses. Primary structure of a muri A;Reference number: A26237; MUID:78242288; PMID:98524

A;Reference number: A26237; MUID:78242288; PMID:98524

A;Contents: annotation; MOPC 21

A;Note: this is the final paper in a series reporting the protein sequence, A;Note: there are a number of differences from the sequence shown
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A;Residues: 170-275,'D',277,'D',279-322 <ROG>
A;Cross-references: GB:V00795; NID:g51830; PIDN:CAA24176.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 76-324 <OBA>
A;Cross-references: GB:V00775; NID:951652; PIDN:CAA24153.1;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTQKSLSLSP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLOSDLYTLSSSVTVPSSP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS
                                                                                                                                                                                                                                                                                                                                                                                                            431
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Pred. No. 7.5e-43;
50; Mismatches 60;
                                           (TMV) inactivating neotop
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                                                                                              H.J.; Kreuzaler,
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S

LW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142

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A;Molecule type: DNA
A;Residues: 138-172, P',174-189, FP',193-376, T',378-474
R;ORIO, R.; Rougeon, F.
Nature 296, 761-763, 1982
N;Title: Mouse immunoglobulin allotypes: post-duplication
A;Title: Mouse immunoglobulin allotypes: post-duplication
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b_allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 138-161,'L',163-189,'FP',193-474
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associa C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; if;157-222/Domain: immunoglobulin homology <IMI> F;137-227/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TUI>A;Note: Lys-474 is probably removed posttranslationally R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattne Science 206, 1303-1306, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; I: J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b A;Reference number: A53598, MUID:94216359; PMID:7512967
A;Accession: A53598
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                                                                                                                                                                                                                                                                                  F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Comment: The a allele sequence is shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A;Cross-references: GB:J00461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A26232; MUID:80081502; PMID:117549 A;Accession: A26232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: MPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Structure of the constant and 3' v A; Reference number: A26235; MUID:80081501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete nucleotide sequence of immunoglobulin A;Reference number: A02157; MUID:80120716; PMID:6766534 A;Contents: a allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 234-251 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A26233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Sequence of the cloned gene for the constant region of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A26235
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                                                                                                                                                                                                                                                        ;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Introns: 138/1; 236/1; 258/1; 368/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                           Local Similarity
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GASVKMSCKASGYTFITYVMHW-----VKOKPGOGLEWIGYINPNKDGTKFNEKFKGKAT
                                                              GDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG----SFL--TKGPSKLNDRADSRRS 85
                                                                                                                                                           33.9%;
                                                                                                                          ; Score 818; DB 1; I pred. No. 1.3e-42; 66; Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      untranslated; PMID:117548
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Ig gamma-2a chain C region, Burrell Greening (Species: Mus musculus (house mouse)
C;Species: 30-Sep-1980 #sequence revision 01-Sep-1981 #text_change
C;Accession: A02152; A32657; A32658
R;Sikorav, J.L.; Auffray, C.; Rougeon, F.
Nucleic Acids Res. 8, 3143-3155, 1980
A;Title: Structure of the constant and 3' untranslated regions (house)
A;Title: Structure of the constant and 3' untranslated regions (house)
A;Contents: annotation; myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence;
A;Note: this sequence differs from that shown at a number of gride Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gan A;Reference number: A32660; MUID:73056887; PMID:4565406
A;Contents: annotation; MOPC 173, disulfide bonds
C;Genetics:
                                                                                                                                                                                                                                        A;Residues: 1-330 <OLL>
A;Note: the sequence was determined from the germline gene A;Note: Lys-330 is removed posttranslationally R;Bourgois, A.; Fougereau, M.; Rocca-Serra, J. Euchem. 43, 423-435, 1974
A;Title: Determination of the primary structure of a mouse A;Reference number: A32659; MUID:74175517; PMID:4831970
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: the sequence was determined from the germline gene R;0110, R.; Auffray, C.; Morchamps, C. Rougeon, F. Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2464, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests A;Reference number: A32658; MUID:81223894; PMID:6787604
A;Accession: A32658; MUID:81223894; PMID:6787604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:V00798; NID:g51835; PIDN:CAA24178.1; PID:g1 R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin A;Reference number: A32657; MUID:81198976; PMID:6262729
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A; Residues: 1-330 < YAM>
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A; Residues: 1-330 <SIK>
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                                                                                 gammaG2a immunoglobulin.
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A; Molecule type: protein
A; Residues: 118-267, 'E',269-328, 'G',330-334 < DOG>
A; Residues: 118-267, 'E',269-328, 'G', 330-334 < DOG>
C; Comment: Lys-335 is removed posttranslationally.
C; Comment: The sequence differs from that of the a allele, from BALB/c mice, at 15% of t C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IGA and IgM, the subunits associate into la C; Superfamily: immunoglobulin cregion; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F; 20-84/Domain: immunoglobulin homology < IM1>
                                                                                                                                                                                                                                                                                                                                                                                                          R;Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 1 C;Accession: A02153; A12656 R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981 A;Title: Multiple differences between the nucleic acid sequences A;Reference number: A02153; MUID:82037861; PMID:6170065
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1s C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;20-84/Domain: immunoglobulin homology <IM1>
                              F;248-315/Domain: immunoglobulin F;15/Disulfide bonds: interchain
                                                                                     F;98-118/Region: hinge F;142-211/Domain: immur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A02153;
A;Accession: A02153
A;Molecule type: mRNA
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology calM3>
F;15/Disulfide bonds: interchain (to light chain) #status experimental
F;27-82,144-204,250-308/Disulfide bonds: #status experimental
F;107,110,112/Disulfide bonds: interchain (to heavy chain) #status exp
F;180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain C57BL/6
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C;Species: Mus musculus (house mouse)
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Best Local Similarity
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                                                                                        immunoglobulin homology <IM2>
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homology <IM3>
(to light chain)
bonds: #status [
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                              #status
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A;ACCESSION.
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Residues: 1-475 <DE1>
A;Coss-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Coss-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <NAT>
F;20-475/Product: Ig gamma-2b ohain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>
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R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: $01320; MUID:88329081; PMID:3138116
A;Accession: $01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Dsecies: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
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Best Local
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Similarity 40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LELQDSGTW-----TCTV-----LQNQKKVEFKIDIV--PCPAPEPKSCDKTHTCPELL
PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCP---
                                                                   TLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF
                                                                                                      LTLTLESPPGSSPSVQ-----CRSPRGKNI------
                                                                                                                                        GKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA---GPRQVGLLPFG-----YWGQG
                                                                                                                                                                            SRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                                                                                                             LARPGASVKLSCKASGYTLTSYGISW-----VKQRTGQGLEWIGEIYPGSGNSYFNEKFK
                                                                                                                                                                                                                                                 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD
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                             SQLELQDSGTW----TCTVLQ--NQKKVEFKID-----IVPCPAPE
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                                                                                                                                                                                                                                                                                                       Score 793.5; DB 2;
Pred. No. 3.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 801; DB 1;
Pred. No. 9.1e-42;
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R.Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: D25941
A;Status: preliminary
A;Molecule type: DNAY
A;Molecule t
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Gene 74, 473-482, 1988

A; Title: Evolution of the rat immunoglobulin gamma heavy-chain A; Reference number: PS0017; MUID:89232738; PMID:3149946

A; Accession: PS0019
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C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990
C;Accession: PS0019; D25941
R;Bruegraman "
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C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobuli:
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A; Residues: 1-322 <BRU>
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                                              HNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
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   HNHHTEKSLSHSPG
                                                                                                                                                                       YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
                                                                                                                                                                                                                                                        WLNGKTFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTMAPPKEEMTQSQVSITCMVKGF
                                                                                                                                                                                                                                                                                                                    WLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGF
                                                                                                                                                                                                                                                                                                                                                                                       ITLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVHRD
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                                                                                                                            YPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKETWQQGNTFTCSVLHEGL
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Pred. No. 2.9e-41;
""" matches 72;
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A; Cross-references: GB:M31134
C; Comment: This protein is expressed on most thymocytes, on a subset of matic comment: This protein is expressed on most thymocytes, on a subset of comment: This protein is expressed on most thymocytes, on a subset of matic comment: The comment of the comment
                                                                                                                                   A;Note: the sequence was d
C;Genetics:
A;Gene: IG CH gamma 2
A;Introns: 99/1; 112/1; 21
C;Superfamily: immunoglobu
C;Keywords: glycoprotein;
F;20-85/Domain: immunoglob
F;175/Binding site: carboh
                                                                                                                                                                                                                                                                                                                                                           A;Accession.
A;Molecule type: DNA
A;Residues: 1-327 <SYM>
A;Cross-references: EMBL:X16702
A;Cross-reference was determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-2 chain C region (clone 32.2) - bovine (fragment) (Species: Bos primigenius taurus (cattle) (C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_c C;Accession: $06611; B31303 R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Macaca mulatto
C;Date: 30-Sep-1993 #seq
C;Accession: C32722
R;Camerini, D.; Seed, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024 A;Accession: C32722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell surface glycoprotein CD4 - rhesus macaque
N,Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
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S06611
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A; Residues: 1-432 < CAM>
   Query Match
Best Local S
Matches 146
                                                                                                                                                                   Superfamily: immunoglobulin C region; immunoglobulin homology; Keywords: glycoprotein; immunoglobulin; membrane protein; 20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 152;
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Best Local S
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                                   Local Similarity
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                                                                                                                                      carbohydrate (Asn)
                                   32.1%;
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Score 774; DB 2;
Pred. No. 3.9e-40;
1; Mismatches 55;
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Pred. No. 5.7e-41;
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                                                               Length 327;
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R.Hague, B.F.; Sawasdikosol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; Kindt, Proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
A;Title: CD4 and its role in infection of rabbit cell lines by human immunoc A;Reference number: A46254; MUID:92390370; PMID:1518821
A;Accession: A46254
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-459 <HAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
146732
A;Cross-references: GB:M92840; NID:g164871; PIDN:AAA31198.1; A;Note: sequence extracted from NCBI backbone (NCBIN:112732, C;Superfamily: T-cell surface glycoprotein CD4; immunoglobuli
                                                                                                                                                                                                    C;Species: Oryctolagus cuniculus (domestic C;Date: 21-Sep-1993 #sequence_revision 18-NC;Accession: A46254
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A;Molecule type: mRNA
A;Residues: 1-180 <HEI>
A;Cross-references: GB:J00665; NID:g165109; PIDN:AAA31288.1; PID:g165110
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;93-160/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 10, 1535-1545, 1982 A;Title: Molecular cloning of rabbit gamma A;Reference number: I46732; MUID:82174328; A;Accession: I46732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: I46732
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL
                                                                                                                                                                                                                                                                                                                                                                                                                              PAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALHNHYTOKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 702; DB 2;
Pred. No. 4.8e-36;
6; Mismatches 28
                                                                                                                                                                                                                       stic rabbit)
18-Nov-1994
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PMID:6280149
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                     PID:g164872
NCBIP:112733)
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RESULT 44
S30193
T-cell surface
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(;Species: Homo sapiens (man)
(;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 21-Jan-2000
(;Accession: A36040
R,Eulitz, M.; Weiss, D.T.; Solomon, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 6542-6546, 1990
A,Title: Immunoglobulin heavy-chain-associated amyloidosis.
A,Reference number: A36040; MUID:90370821; PMID:2118650
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A36040
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A;Accession: A36040
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Best Local :
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                                                                                             CSVMHEALHNHYTQKSLSLSPG 431
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                                                                            CSVMHEGLHNHYTQKSLSLSPG
                                                                                                                                      LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
                                                                                                                                                      LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
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                                                                                                                                                                                                                               VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 349
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77.5%;
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41.9%; Pred. No. 1.9
   CD4
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Pred. No. 3.5e-28;
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C;Species: Canis lupus familiaris (dog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S30193
R;Milde, K.F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A;Title: Primary structure of the canine CD4 antigen.
A;Reference number: S30193; MUID:93192324; PMID:7916632
A;Accession: S30193
A;Accession: S30193
A;Status: preliminary
A;Molecule type: mRMA
A;Residues: 1-432 <MIL-
A;Cross-references: EMBL:X68565; NID:9288652; PIDN:CAB37664.1; PID:94467377
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: glycoprotein
F;202-311/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                              Ig heavy chain VHIII-D-JH-CH3 region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
C;Accession: S69340
R;Khamllchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262689; PMID:7744049
A;Accession: S69340
                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residuse: 1-249 <KHA>
A;Residuse: 1-249 <KHA>
A;Crose-references: EMBL:X81696
C;Superfamily: immunoglobulin C r
F;162-229/Domain: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 300
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23.7%;
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                                                             homology < IMM>
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Pred. No. 7.7e-28;
1; Mismatches 127;
Score 572.5; DB 2
Pred. No. 5.4e-28;
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Best Local Similarity

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RESULT 47
A27449
A;Molecule type: mRNA
A;Residues: 1-457 <CLA>
A;Residues: GB:M15768; NID:g203387; PIDN:AAA40901.1;
A;Cross-references: GB:M15768; NID:g203387; PIDN:AAA40901.1;
A;Cross-references: GB:M15768; NID:g203387; PIDN:AAA40901.1;
A;Pavis, S.J.; Ward, H.15768; NID:g203387; PIDN:AAA40901.1;
J. Biol. Chem. 265, 10410-10418, 1990
A;Title: High level expression in Chinese hamster ovary cells
A;Reference number: A35433; MUID:90285164; PMID:2113054
                                                                                                                                       T-cell surface glycoprotein CD4 precursor - rat
N;Alternate names: W3/25 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Jan-2000
C;Accession: A27449; A3543
R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987
A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: eviden A;Reference number: A27449; MUID:87175535; PMID:3104900
A;Accession: A27449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-152 <VAN>
A;Residues: 1-152 <VAN>
A;Cross-references: EMBL:X56393; NID:g51617; PIDN:CAA39804.1; PID:g51618
C:Superfamily: immunoglobulin C region; immunoglobulin homology
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C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_cha
C;Accession: S14236
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant
A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14236
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C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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Pred. No. 7.6e-28;
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A;Concents: annotation C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin C;Keywords: glycoprotein; membrane protein; surface antigen F;219-300/Domain: immunoglobulin homology <IMM>
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----PQVSLQFAGSG----NLTLT----LDR-GILYQEVNLVVMKVTQPDSNTLTCEVM
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::
                               GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355
                                                                                                                                                                                                            DSGIWNCTVTLNQKKHSFDMKLSVL-----GFASTSITAYKSEGESAEFSFP-----
                                                                                                                                                                                                                                           DSGTWTCTVLQNQKKVEF--KIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                       LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.5%;
                                                                                                                                       -LNLGEESLQGELRW-----KAEKAPSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 495; DB 2;
; Pred. No. 5.7e-23;
57; Mismatches 132
                                                                   --VQKSTSNPKFQLSE----TLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                   ---LTLQI-
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331
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A;Molecule type: DNA
A;Residues: 1-25, 'E', 27-457 <GOR>
A;Cross-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; E
A;Crosd-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; E
R;Maddon, P.J.; Molineaux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey,
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
A;Title: Structure and expression of the human and mouse T4 genes.
A;Reference number: A39955; MUID:88097446; PMID:3501122 A; Molecule type: mRNA
A; Residues: 1-457 <LIT>
A; Cross-references: GB: X04836; NID: g50353; C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. R;Gorman, S.D.; Tourvieille, B.; Parnes, J.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
A;Title: Structure of the mouse gene encoding CD4 and an
A;Reference number: A39893; MUID:88041159; PMID:2823269 A; Accession: A26038 A; Title: Unusual intron in the immunoglobulin domain of A; Reference number: A26038; MUID:87115821; PMID:3027575 A;Cross-references: GB:M13816; R;Littman, D.R.; Gettner, S.N. Nature 325, 453-455, 1987 A; Molecule type: mRNA A; Residues: 1-457 < TOU> Science 234, 610-614, 1986
A;Title: Isolation and sequence of L3T4 complementary DNA
A;Reference number: A02110; MUID:87018845; PMID:3094146
A;Accession: A02110 T-cell surface glycoprotein CD4 precursor - mouse N; Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen A;Accession: A39893 NID:g192070; PIDN:AAA37267.1; PIDN: CAA28539.1; the unusual transcript in clones: expression PID:g50354 newly isolated PID:g309112 PID:g387124 M.; Alt, F murine ij brain T4/Leu н **9** cells Σ

F

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RESULT 49
B46529
Ig Y heavy chain (7.8S) - duck
Ig Y heavy chain (7.8S) - duck
N;Alternate names: Ig gamma chain (7.8S)
C;Species: Anas platyrhynchos (domestic duck)
C;Sate: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B46529; S20759
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 208-318 <a href="RE2">RE2">RESIDUES: 208-318 <a href="RE2">RESIDUES: 208-318 <a href="RE2">RECOURSE: CEFECTECES: GB:M36851; NID:g198672; R; Classon, B.J.; Tsagaratos, J.; Kirszbaum, Immunogenetics 23, 129-132, 1986
A; Title: The L3T4 antigen in mouse and the s. A; Reference number: A47642; MUID:86166694; P. A; Accession: A47642
A; Accession: A47642
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F;220-301/Domain: immunoglobulin homology <IM3>
F;241-457/Product: CD4, brain-specific short form #status prediction for immunoglobulin homology <IM4>
F;321-372/Domain: immunoglobulin homology <IM4>
F;395-419/Domain: transmembrane #status predicted <IM7>
F;420-457/Domain: intracellular #status predicted <INT>
F;420-457/Domain: intracellular #status predicted <IM7>
F;420-112,159-188,328-370/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2 (;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; tF;1-26/Domain: signal sequence #status predicted csIG> F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental < F;35-114/Domain: immunoglobulin homology < M1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 27-43 < CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-457 < RES>
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A; Residues: 25-457 < MAD>
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Best Local S
Matches 104
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                                                                                                                                                                                                                                                                                                                                VQDSDFWNCTVTLDQKK 196
                                                                                                                                                                                                                                                                                                                                                                                      LODSGTWTCTVLQNQKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCRAISLRRLLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 475; DB 1; 52.8%; Pred. No. 9.5e-22; tive 32; Mismatches 55
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PMID:3082751
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L.; Maddox, J.; !
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Mackay, C.R.; Brandon,
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Ig heavy chain precursor - African clawed frog (fragment c)Species: Kenopus laevis (African clawed frog) C;Species: Kenopus laevis (African clawed frog) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text C;Accession: S04845; S05695 R;Ameniya, C.T.; Haire, R.N.; Litman, G.W. Nucleic Acids Res. 17, 5388, 1989 Nucleic Acids Res. 17, 5388, 1989 A;Title: Nucleotide sequence of a cDNA encoding a third A;Reference number: S04845; MUID:89345103; PMID:2503814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin C region; immuno
C;Keywords: immunoglobulin
F;37-120/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: spleen A; Note: sequence extracted from
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A; Residues: 1-572 < MAG>
δ
                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 'LC',3-308,'H',310-549 <LIT>
A;Cross-references: EMBL:X15114; NID:964799; PID:9763031
C;Superfamily: immunoglobulin C region; immunoglobulin h
                                                                                                                                                                                                                                                                           A; Reference number: S05695
A; Accession: S05695
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                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-549 < AME>
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                                                                                                                                                 ;Keywords: glycoprotein; heterotetramer; immunoglobulin;26-109/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: EMBL:X15114
                                          Matches
                                                            Query Match
Best Local
                                                                                                                            281,294/Binding site:
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                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGKNIQGGKTLSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDSVELLCVITGFSPPPVEVEWLVDGAPAH------LVATMTRPQ------REA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDSDTYICEV---EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFLYSKMTVPKASWQGGVSYACMVVHEGLPMRFTQRPLQKTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFTFPPHAEELSLAEVTLTCLVRGFQPEHVEVQWLRNHNSVPAAEFVTTPPLKEPNGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW--ESNGQPENNYKTTPPVLD--SDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPMVLTEHFNGTFTASSSLAISTODWLAGERFTCTVQHEDLPVPLGKSIAKHAGKVTAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I-----QIFVVPPSP-GSLYIRQDAKVHCLVVNLP-SDASLSISWTREKSGALRP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
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                                                                                                                                              immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                          Conservative
--NFPLIIK------NLKIEDSD----
                                                                                                                            carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.0%;
30.0%;
                                                              16.7%;
29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 411.5; DB 2; ; Pred. No. 9.1e-18; 55; Mismatches 136;
                                          65,
                                     Score 402.5; DB 2;
Pred. No. 3.1e-17;
5; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin
                                                                                                                            (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (fragment)
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                                                                                                                            #status predicted
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                                          Indels
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                                                                                    549;
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                                          ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus immunoglobulin
                                          Gaps
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112
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                                          17;
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482

597

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Ig mu chain precursor, membrane-bound (clone 201) - human C;Species: Homo sapiens (man)
C;Species: Al-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: S1683; S08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Tille: Complete nucleotide sequence of the membrane form of the human IgM |
A;Reference number: S14683; MUID:9032450; PMID:2115996
A;Reference number: S14683; MUID:90332450; PMID:2115996
A;Residues: 1-627 <FRI>A;Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:933451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>F;1-15/Domain: signal sequence #status predicted <MAT>
F:36-627/Product: Ig mu chain #status predicted <MAT>
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S14683
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Best Local S
Matches 116
  273
                                         377
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                                                                                                                                                                                                                                                                                             210 SVLRGGKYAATSQVLLPSKD-------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 CQDEPEPIEPTVEILQGPCASSKSVELLCLITGYAPSEIKVHWLLNGQ---VTNISPSNS
                                                                                                                                                                                                                                                                                                                                  94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL-----QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                      36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEGFISFSKLTIARSDWMRGATYSCI----AAHNTISQRDIKKNRG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EASTKKCDETAITPKVDVLPPSPKD-LLVTKEAKVYCVISRMASTD-DLTVQWSRSDGKK
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REP 331
                                                                                 THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                        AEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR 376
                                                                                                                                                                    LELODSG-----
                                                                                                                                                                                                            AELPPKVSVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG--QPENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALAFDSAP-EKAYDGTFTVKSTLKISPGDWENKKQFNCKVVHPDLPSPIEKSIQKSQDPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KP---CKEENG-TFSSRSKVSVPKEDWNSEDSYTCKVTH-------PASHTKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEPTITLLPPSDDELRNDFISLICMLKNFRPQDIYVFWKKDGVTLEEDYYMTTTPVLEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.1%; Score 389; DB 2; ]
23.9%; Pred. No. 2.4e-16;
ative 77; Mismatches 167;
                                                                                                                                                              ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                   GKNIQGGKTLSVSQ 173
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A;Title: Cloning and nucleotide sequence of mouse immunoglobulin A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Accession: A02144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A02144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SD 386
                                       HSTTTP-LKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLG
                                                                                                                                              EKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN--
                                                                                                                                                                                                                                                 ----WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                              AQTVLIKE-EGKLASTCSKLNITEQQWMSESTFTCKV--TSQGVDYLAHTRRCPDHEPR-
                                                                                                                                                                                                                                                                                                                                                                                                                    SPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVNITEPTLELLHSSCDPNAFHSTIQLYCFIYGHILNDVSVSWLMDDREITDTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLKIEDSDTYI----CEVEDQKEEVQL--LVFGLTAN--SDTHLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIK 97
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                                                                            YKTTPPVLDSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG
                                                                                                                      VRSITKTPGQRSAPEVYVFPPPEEE-SEDKRTLTCLIQNFFPEDISVQWLGDGKLISNSQ
                                                                                                                                                                                                                                                                                                                                  CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELKVTTSQVTS----WGKSAK----NFTCHVTHPPSFNESRT-----ILVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS----TEGEVSADEEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGEL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 388; DB 1;
28.3%; Pred. No. 1.6e-16;
ative 77; Mismatches 138
                                                                                                                                                                                                                                                                                           -GVITYLIPPSPLD-LYQNGAPKLTCLVVDLESEKNVNVTWNQEKKTSV
                                                                                                                                                                                                       NATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 388
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169

261

381 431 322 375 263 149

59

113

epsilon chain cDNA

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RESULT 54

$3,7768

$3,7768

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change

C; Accession: $3,7768
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Nucleic Acids Res. 19, 2427-2433, 1991
A; Title: mRNA transcripts initiating within
A; Reference number: $15590, MUID:91252286; P
A; Accession: $15590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
S15590
A;Title: Comparison of complete nucleotide A;Reference number: S37767; MUID:93109369; A;Accession: S37768 A;Accession: S37768 A;Molecule type: mRNA
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A;Note: the authors translated the codon CF
C;Superfamily: immunoglobulin C region; imm
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: mRNA
                                                                               R; Harindranath,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g heavy chain - human
;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                 rindranath, N.; Donadel, G.; Sigounas, Immunol. 30, 111-112, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                          446
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                                                                                                                                                                                                                                                                                                                                                                                              VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELQDSG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESPPGSSPSVQCR------SPR-----GKNIQGGKTLSVSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLRGGKYAATSQVLLPSKD-------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                           VYLLPPAREQLNLRESATITCLVTGFSPADVFVQMMQRGQPLSPEXYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                             TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
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23.7%; Pre
78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 386.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n CAA for residue 265 as Glu
immunoglobulin homology
                                   sequence of the PMID:8417370
                                                                                  G.; Notkins, A.L.
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PMID:1904154
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                                                   IgM heavy
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                                                   chain
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A;Residues: 1-453 <HAR>
A;Cross-references: EMBL:X67301; NID:g38407; PIDN:CAA47714.1; PID:g38408
A;Cross-references: EMBL:X67301; NID:g38407; PIDN:CAA47714.1; PID:g38408
A;Experimental source: cell line Ab 63
C;Genetics:
A,Map position: 14q32
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;21-90/Domain: immunoglobulin homology <IMM2>
F;217-199/Domain: immunoglobulin homology <IMM2>
F;217-199/Domain: immunoglobulin homology <IMM4>
F;217-199/Domain: immunoglobulin homology <IMM4>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;344-9197,244-303,351-413/Disulfide bonds: #status predicted
F;36,209,272,279,440/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;214,452/Disulfide bonds: interchain (to heavy chain) #status predicted
F;214,452/Disulfide bonds: interchain (to heavy chain) #status predicted
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Best Local Similarity
  398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVELTCTASO--KKSIOFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                            LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                     REQUNIRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI
                                                                                                                               RDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSK 394
                                                                                                                                                                           PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                                                                                                                     YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
                                                                                                                                                                                                                                                                     ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                             GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                         TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-----
                                                                                                                                                                                                                                                                                                                                                                                                     -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG
LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
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Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SPR------GKNIQGGKTLSVSQLELQDSG-
                                            431
  434
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Ig mu Chain - sheep

Ig mu Chain - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic she

C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change

C;Accession: S25705

R;Patri, S; Nau, F

Mol. Immunol. 29, 829-836, 1992

A;Title: Isolation and sequence of a cDNA coding for the immunos

A;Reference number: S25705

A;Accession: S25705

A;Accession: S25705

A;Accession: S25705

A;Residues: preliminary

A;Residues: 1-592 <PATY

A;Cross-references: EMBL:X59994; NID:g1269; PIDN:CAA42611.1; PII

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin C region; campaid companies immunoglobulin homology

F;483-554/Domain: immunoglobulin homology <IMMY
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immunoglobulin mu

chain

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PID: 91270

sheep) nge 23-Jul-1999

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A; Molecule type: DNA
A; Residues: 1-39,'L', 41-432,'GKPTLYNVSLVMSDTAGTCY' < DOR3>
A; Cross-references: EMEL: X14940
R; Rabbitte, T.H.; Forster, A.; Milstein, C.P.
Nucleic Acids Res. 9, 4509-4524, 1981
A; Title: Human immunoglobulin heavy chain genes: evolutionary
A; Reference number: A26243; MUID: 82059479; PMID: 6795593
A; Accession: B26243
A; Molecule type: DNA
A; Residues: 433-436,'N',438,'E',440-447,'T',449-473 < RAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo Sapiens (man)
C;Date: 29-Jan-1993 #sequence revision 23-Aug-1997 #text_change 22-C;Date: 29-Jan-1993 #sequence revision 23-Aug-1997 #text_change 22-C;Accession: S16510; S09357; S16656; B26243; A02167
R;Doral, H.; Gillies, S.D.
Nucleic Acids Res. 17, 6412, 1989
A;Title: The complete nucleotide sequence of a human immunoglobulin A;Reference number: S09357; MUID:89366690; PMID:2505237
A;Accession: S16510
                                                                                                                                                                                                                             A; Reference number: A; Accession: S16656
                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: S16656
                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-432, 'GKPTLYNVSLYMSDTAGTCY' <DOR2>
A;Crose-references: EMBL:X14940
A;Note: the authors translated the codon AAT fo
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X14939
A;Note: the authors translated the codon AAC for residue 445 as Met
A;Note: the sequence of residues 1-432 was assumed to be identical with
A;Accession: S09357
                                                                                                                                                                                                                                                                                               R;Dorai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 433-473 < DOR1>
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Best Local Sim.
Matches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSLTLTLESPPGSSPSVQCR----SPR-----GKNI-----QGGKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VALHSSSTFQGTDGYLVCEVQHPKGEDVGHKGVPREVEVLSPVVSVFVPPCNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLIIKNLKIEDSDTY-ICEVEDQK-----EEVQLL-----VFGLTANSDTHLLQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVTEEDWSKGETYTCVVGHEALPHMVTERTVDKSTG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQLSLRESASVTCLVKGFAPADVFVQWLQKGEPVAKSKYVTSSPAPEPQDPSAYFVHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELT-KNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFTIPPSFAD-IFLTKSAKLSCLVTNLASYD-GLNISWSHQNGKALETHTY----FERHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELEBEKEKDTLMISRTPEVTCVVVDVSHEDBEVKENW-YVDG--VEVHNAKTKEREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYSVLTITEREWLSQSAYTCQVEHNKETFQKNAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDTFSARGEASVCSEDWESGEEYTCTVAHLDLPFPEKSAISKPKDVAMKPPSVYVLPPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LSGNGNSKSSLICQATDFSPKQISLSWFRDGKRIVSDISEGQVETVQSSPTTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
                                                                                                                                                                                                                                                                                                                   splice form
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Pred. No. 4.5e-16;
                                                                                                                                                                                                                                                                        April
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F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM3>
F;445/Domain: immunoglobulin homology <IMM4>
F;433-473/Domain: immunoglobulin homology <IMM4>
F;443-473/Domain: carboxy1-terminal #status predicted <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;28-88,134-197,244-303,351-413/Disulfide bonds: #status experimental
F;46,209,272,279/Binding site: carbohydrate (Asm) (covalent) #status experimental
F;214/Disulfide bonds: interchain (to mu chain in another subunit) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 14q32.33-14q32.33
A;Introns: 1/1; 105/1; 217/1; 323/1; 433/1; 471/3
C;Complex: An immunoglobulin heterotetramer subunit consists of hain disulfide bonds. The IgM subunits associate into disulfide c;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; glycopyotetin; heterotetramer; F;21-90/Domain: immunoglobulin homology <IMM1:
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A; Cross-references: GDB:120086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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445
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NLWAT
                                                GLWTT 452
                                                                                             RYFAHSILTVSEEEWNTGETYTC-VAHEALPNRVTERTVDKS----TEGEVSADEEGFE
                                                                                                                                           SFFLYSKLTYDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                                                                                                                                                                                    VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LESPPGSSPSVQCR------SPR-----GKNIQGGKTLSVSQL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVLRGGKYAATSQVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                           VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                           TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
                                                                                                                                                                                                                                                                                                                                      TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAKESGPTTYKVTSTLTIKESDWLGQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELQDSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
                                                                                                                                                                                                                                                                                                                                                                                            -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
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  449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 381; DB 1; Length 473
Pred. No. 5.2e-16;
7; Mismatches 166; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of
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R;Kipp, B.; Becker, W.; Schlaak, M. submitted to the EMBL Data Library, November 1993 A;Description: Combination of a defined specificity

Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C;Accession: S38864

#text_change

24-May-2001

and desired isotype

by cloning of

S38864

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A; Molecule type: DNA
A; Residues: 1-39, L', 41-452 < DOR2>
A; Cross-references: EMBL:X14940
R; Harindranath, N.; Donadel, G.; S
Mol. Immunol. 30, 111-112, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-452 <DOR1>
A;Cross-references: EMBL:X14940
A;Note: the authors translated the R;Dorai, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Dorai, H; Gillies, S.D.

Nucleic Acids Res. 17, 6412, 1989

A;Title: The complete nucleotide sequence of a human immunoglobulin genomic C-mu A;Reference number: S09357; MUID:89366690; PMID:2505237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo Sapiens (man)
C;Species: Homo Sapiens (man)
C;Date: 29-Jul-1981 #sequence_revision 23-Aug-1997 #text_change 22-Jun-1999
C;Date: 29-Jul-1981 #sequence_revision 23-Aug-1997 #text_change 22-Jun-1999
C;Date: 29-Jul-1981 #sequence_revision 23-Aug-1997 #text_change 22-Jun-1999
A; Title: Human immunoglobulin heavy chain genes: evolutionary A; Reference number: A26243; MUID:82059479; PMID:6795593
                      A;Cross-references: EMBL:X67292; NID:g38405; I
R;Rabbitts, T.H.; Forster, A.; Miselin, C.P.
Nucleic Acids Res. 9, 4509-4524, 1981
A;Title: Human immunoglobulin heavy chain gen
                                                                                                                                                                                               A; Title: Comparison of complete nucleotide A; Reference number: S37767; MUID: 93109369; A; Accession: S37767
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A;Residues: 1-548 <KIP>
A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A;Accession: S38864
A;Status: preliminary
                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-190, 'S', 192-414, 'V', 415-452 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S16656
A; Accession: S16656
                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, April 1989
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                                                                                                                                                                     A; Status: preliminary
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PMID:8417370
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A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 1493:33-1493:33
A;Introns: 1/1; 105/1; 217/1; 323/1; 433/1
C;Complex: An immunoglobulin heterotetramer subunit consists of hain disulfide bonds. The IgM subunits associate into disulfide C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; glycoprotein; heterotetramer; F;21-90/Domain: immunoglobulin homology cIMMIN consists of the property of the property
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A, Title: Cloning of human immunoglobulin mu gene and co A, Reference number: 137748; MUID:81124312; PMID:6450943 A, Status.
F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;432-452/Domain: immunoglobulin homology <IMM4>
F;432-452/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;28-88,134-197,244-303,351-413/Disulfide bonds: #status experimental
F;46,209,272,279,439/Binding stee: carbohydrate (Asn) (covalent) #status experimental
F;214,451/Disulfide bonds: interchain (to mu chain in another subunit) #status experimental
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A; Molecule type: protein
A; Residues: 100-144, E', 146-162, 'E', 164, 'E', 166-214, 'G', 216-262, 'D', 264-295, 'D'
A; Note: all four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms
R; Watanabe, S.; Barnikol, H.U.; Horn, J.; Bertram, J.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1505-1509, 1973
A; Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-17;105-186;200-259;296-322;339-416,'D',418-452 <RAB>
A;Cross-references: GB:K01310; NID:g184715
A;Cross-references: GB:K01310; NID:g184715
A;Dolby, T.W.; Devuono, J.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 77, 6027-6031, 1980
A;Title: Cloning and partial nucleotide sequence of human immunoglobulin A;Reference number: A26244; MUID:81077306; PMID:6777778
A;Reference number: A26244; MUID:81077306; PMID:6777778
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A;Cross-references: EMBL:V00563; NID:g33454; PIDN:CAA23826.1; PID:g825684
R;Cross-references: EMBL:V00563; NID:g33454; PIDN:CAA23826.1; PID:g825684
R;Mihaesco, E.; Barnikol-Watanabe, S.; Barnikol, H.U.; Mihaesco, C.; Hilschmann,
Eur. J. Blochem. 111, 275-286, 1980
Eur. J. Blochem. 111, 275-286, 1980
Eyr. J. Barnikol, H.U.; Mihaesco, C.; Hilschmann, Eyr. J. Blochem. 111, 275-286, 1980
Eyr. J. Barnikol, H.U.; Mihaesco, C.; Hilschmann, Eyr. J. Barnikol, H.U.; Mihaesco, Eyr. J. Barnikol, H.U.; Mihaesco, C.; Hilschmann, Eyr. J. Barnikol, H.U.; Mihaesco, Eyr. J. Barnikol, H. J. Barnikol, H.U.; Mihaesco, Eyr. J. Barnikol, H.U.
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A; Cross-references: GB: J00257; NID: g185053; PIDN: AAA53508.1;
A; Cross-references: GB: J00257; NID: g185053; PIDN: AAA53508.1;
A; Cross-references: GB: J00257; NID: g185053; PIDN: AAA53508.1;
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A;Note: this sequence has been revised in reference A02162
R;Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-17,'BPS',22,'T',24-82,'N',84-90,'Z',92-93,'B',95,'B',97-144,'E',146-162,'E'
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Science 182, 287-291, 1973
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A;Accession: I37750
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experimental

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Ig heavy chain C region - African clawed frog (fragment) C;Species: Xenopus laevis (African clawed frog) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change C;Accession: S03186 R;Haire, R.N.; Shamblott, M.J.; Amemiya, C.T.; Litman, G.W. Nucleic Acids Res. 17, 1776, 1989 A;Title: A second Xenopus immunoglobulin heavy chain constant re A;Reference number: S03186 A;Accession: S03186
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A;Note: the authors translated the codon TTT for residue 9 as Ser and C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-448 <HAI>
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                           HGQIKVKWLVNGKQDVSAEASVPTPSKTEDGTYSSSSQLRIL-KGMWNKGTQYSCIVTHT
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QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP---
                                                                                                                                                                                                                                                         ADSRRSLWDQGNFPLIKNLK--IEDSD------TYICEV----EDQ 114
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                                                                                                                                         KQEKSLKVLPCMA------PHVQLFLQSPCMSDAISRAQHENINATLDLLCIINNFY 145
                                                                                                                                                                                                                   ADPLDIQWNDGSITTGIKTMRPVLSDVDGLYTLSSQLTILASEWKNSTYKCKVVHNYTNT
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                   15.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%; Score 376.5; DB 1
24.1%; Pred. No. 9.4e-16;
tive 75; Mismatches 156
                                                                                                  -SVQCRSPRGKNIQGGKTLSVSQLELQDSGTW-----TCTVLQN
                                                                                                                                                                                                                                                                                                                   Score 374; DB 2;
Pred. No. 1.3e-15;
                                                                                                                                                                                                                                                                                                Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TWTCTVLONOKKVEFKIDIVPCPAPEPKSCDKT
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F;129-201/Domain: immunoglobulin homology <IMM2>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: immunoglobulin homology <IMM4>
F;436-476/Domain: immunoglobulin homology <IMM4>
F;436-476/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89,136-199,246-305,353-415/Disulfide bonds: #status predicted
F;46,211,243,258,281/Binding sitte: carbohydrate (Asn) (covalent) #status predicted
F;216/Disulfide bonds: interchain (to mu chain in another subunit) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 410-476 (ROGs)
A;Residues: 410-476 (ROGs)
A;Cross-references: GB:V00821; NID:g52355; PIDN:CAA24202.1; PI
A;Cross-references: GB:V00821; NID:g52355; PIDN:CAA24202.1; PI
R;Kawakami, T.; Takahashi, N.; Honjo, T.
Nucleic Acids Res. 8, 3933-3945, Honjo, T.
Nucleic Acids Res. 8, 3933-3945, PiD: mouse immunoglobulin
A;Title: Complete nucleotide sequence of mouse immunoglobulin
A;Reference number: A02166; MUID:81076590; PMID:6255422
A;Accession: B02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-435,'GKPTLYNVSLIMSDTGGTCY' <KAW>
C;Comment: The sequence of residues 1-409 was assumed to be identical with the correspon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:V00816; GB:J00444; NID:g52343; PIDN:CAA24197.1; PID:g52344 R;Rogers, J.; Early, P.; Carter, C.; Calame, K.; Bond, M.; Hood, L.; Wall, R. Cell 20, 303-312, 1980 Cell 21, 306 R;Title: Two mRNAs with different 3' ends encode membrane-bound and secreted forms A;Reference number: A37517; MUID:80222873; PMID:6771019
A;Contents: MOPC 104E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig mu chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Oct-1980 #sequence revision 30-Jun-1991 #text_change C;Accession: A02167; A37517; B02166
R;Early, P.; Rogers, J.; Davis, M.; Calame, K.; Bond, M.; Wall, Cell 20, 313-319, 1980
A;Title: Two mRNAs can be produced from a single immunoglobulin A;Reference number: A02167; MUID:80222874; PMID:6771020
A;Accession: A02167
                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: alternative splicing; duplication; glycoprotein;
F;21-91/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light
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A; Residues: 436-476 < EAR>
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                                Similarity
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  15.5%;
ilarity 25.2%;
Conservative 8
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  Score 373.5;
Pred. No. 1.5e
97; Mismatches
1.5e-15;
ches 157;
                                                        DB 1;
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VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF---

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F;118-186/Domain: i
F;223-291/Domain: i
F;327-398/Domain: i
F;46,99,170,240,265
                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 'N',169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;19-80/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                DNA 1, 335-343, 1982
A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A;Reference number: A90937; MUID:83182019; PMID:6820340
A;Contents: myeloma IR162
A;Accession: A90937
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Nucleic Acids Res. 10, 6041-6049, 1982
A;Tille: Structure and evolution of the heavy chain from
A;Reference number: A93442; MUID:83064537; PMID:6292865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Residues: 1-429 <HEL>
                                                                                                                                                                                                        ,46,99,170,240,265,369,419/Binding site: carbohydrate
                                                                                                                                  Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                         223-291/Domain: immunoglobulin
327-398/Domain: immunoglobulin
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220 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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                                                                                                                                    88;
                                                                                                                                                     Similarity
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                                                          GKLASTYSRLNITQQQWMSESTFTCKVTSQGE--NYWAHTRRCSDDEPR------
                                                                                             GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST------DIL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAREQUALRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT------LRTGGKYLA
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                                                                                                                                                                                                                         immunoglobulin homology <IM2>
immunoglobulin homology <IM3>
immunoglobulin homology <IM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain LOU/c/Wsl, immunocytoma IR2
ddy, E.P.; Moore, J.M.; Faust Jr., C.H.
                                                                                                                                                   15.3%;
31.5%;
                                                                                                                                Score 370.5; DB
Pred. No. 2e-15;
2; Mismatches 1
                                                                                                                                                                   DB 1;
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                                                                                                                                  102;
                                                                                                                                                                     Length
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A; Residues: 439-479 <BE2>
A; Accession: A02164
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Best Local Similarity
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                                                                                                                                                                                                                             122
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                                                                                                                                                                                                                                                                                                                                                                                                                  123;
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                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                             21
   VVDVSHEDPEVKFNWYVDGVEVHNAKT----
                                        FFDKNVSMSSECSTTPSP----
                                                                                                                                                                                                                                                                                                                                          ALTDGNLVAMG----
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                     -GKNIQGG----
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F;130-202/Domain: immunoglobulin homology <IMM2>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted
F;46,114,212,261,277,284/Binding site: carbohydrate (Asn) (covallent) #status predicted
F;219/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-438, 'GRCTLYNVSLIMSDTASTCY' <BER>
A;Residues: 1-438, 'GRCTLYNVSLIMSDTASTCY' <BER>
A;Residues: 1-438, 'GRCTLYNVSLIMSDTASTCY' <BER>
A;Rote: the sequence of residues 1-438 was assumed to be identical with the corresponding C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cIMM')
F;21-92/Domain: immunoglobulin homology cIMM')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig mu chain C region, membrane-bound form - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 23-Aug-1997 C;Accession: A02165; A02164 R;Bernstein, K.B.; Alexander, C.B.; Reddy, E.P.; Mage, R.G. J. Immunol. 132, 490-495, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Complete sequence of a cloned cDNA encoding rabbit A; Reference number: A02164; MUID:84088930; PMID:6418803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLEVTKALWTOTKOFTCRVIHEALREPRKLERTISKSLG 418
                                                                                 QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 247
                                                                                                                                                                           SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                    VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRDELTKNOVSLTCLVKGFYPSDIAVEW--ESNGOPENNYKTTPPVLDSDGS---FFLYS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHNATTSITSILPVDAKDWIEGEGYQCRVDHPHFPKPIVRSITKAPGKRSAPEVYVFLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT-LPP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GVITYLIPPSPLD-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGSASQRSTK 262
                                                                                                                                                                                                                                                                                                                                                   -SFPVDSELPPNVSVFIPPRDSFSGSGTRKSRLICQATGFSPKQI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 369.5; DB 1;
Pred. No. 2.7e-15;
9; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLARDFLPSSVTFSWSFKNNSEI - - -
                                                                                                                                                                                                                                                             --KTLSVSQLELQDSGTW----TCTV----L 187
----GIQVEPIAPSFADT-FLSKSARLICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
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                                                                                                                                                                                                                                                                                                                                                                                                                                    --SPR-- 159
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--KPREEQYNSTYRVVSVLTVLHQDWLNGK 302

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F;126-196/Domain: immunoglobulin homology <IMM2>
F;334-302/Domain: immunoglobulin homology <IMM3>
F;334-302/Domain: immunoglobulin homology <IMM3>
F;341-412/Domain: immunoglobulin homology <IMM4>
F;30-450/Domain: carboxyl-terminal <CTS>
F;430-450/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;27-87,133-194,241-300,348-410/Disulfide bonds: #status predicted
F;20,206,269,276,437/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;211,449/Disulfide bonds: interchain (to mu chain in another subunit) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 178-450 <WAS>
A;Residues: 178-450 <WAS>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E;20-89/Domain: immunoglobulin homology <IMM1>
E;20-89/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Wasserman, R.L.; Capra, J.D. Science 200, 1159-1161, 1978
A;Title: Amino acid sequence of the Fc region of a canine immunoglobulin A;Reference number: A94246; MUID:78180587; PMID:653360
A;Contents: Moo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jul-1981 #sequence revision 13-Jul-1
C;Accession: A93131; A94246; A02169
R;McCumber, L.J.; Capra, J.D.
Mol. Immunol. 16, 565-570, 1979
A;Title: The complete amino-acid sequence of a A;Title: necession: A93131; MUID:80077682; PMID A;Contents: myeloma protein Moo
A;Accession: A93131
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Best Local Similarity
Matches 119; Conser
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Species: Canis lupus familiaris (dog)
                                                        169
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                                                      LSVSQLELQDSG---
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                                                                                                                                                                   SVLRGGKYVATSQVFLPSVDIIQGTDEHIVCKVRHSBGBKQKBVPLPVM------
                                                                                                                                                                                                                                                                             TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPHMVTERTVDKS----TEGEVGAEEEGFENLWTT 455
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                   TNEVZAZAKZSGPTTYKVTSMLTIQEDAWLSQSVFTCKVEHRGLTFQQNASSM----
                                                                                                                              QGQSLTLTLESPPGSSPSVQCR-----
                                                                                                                                                                                                                                              TVAMGCLARDFLPGSITFSWKYEBLSAINSTRG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                         LTL--PPEVSGFIPPRDAFFGBPRKSQLICQASGFSPRQVWSLRDGKQIESGVT
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                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                     Score 369; DB 1;
Pred. No. 2.7e-15;
                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                    -TWTC-----TVLQNQKKVEFKIDIV
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                                                                                                                              ----SPR-----GKNIQGGKT
                                                                                                                                                                                                                                                                                                                                                       Length 450;
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Best Local (
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A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-391 < BAR> C; Comment: This protein has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Barnikol-Watanabe, S.; Mihaesco, E.; Mihaesco, C.; Barnikol, H.U.; Hilschmann, Hoppe-Seyler's Z. Physiol. Chem. 365, 105-118, 1984
A;Title: The primary structure of mu-chain-disease protein BOT. Peculiar amino-a A;Reference number: A02163; MUID:84184186; PMID:6425189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;43-391/Domain: Ig mu chain C region, secreted f F;65-37/Domain: immunoglobulin homology <IRM1> F;15-243/Domain: immunoglobulin homology <IRM2> F;175-243/Domain: immunoglobulin homology <IRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-41/Domain: pre-C <VAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:120086; OMIM:147020 A;Map position: 14q32.33-14q32.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig mu heavy chain disease protein (Bot) -
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-
C;Accession: A02163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,210,217,378/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 15.1%; Score 365.5; DB 1; Local Similarity 28.0%; Pred. No. 3.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 EVED---QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR---
DIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
                                                   RFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SPR-----GKNIQGGKTLSVSQLELQDSG-----TWTCTVLQN---
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                                                                                                                                                              KLTCLVTDLTTYD-SVTISWTRQDGEAVKTHTNISESHPNATFSAVGEASICEDDWDSGE
                                                                                                                                                                                                                  EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                         GQSMFTCRVDHRGLTFQQNASS---
                                                                                                                                                                                                                                                                                                                                                                                         KLICQATGFSPRQIEVSWLREGKQVGSGVTTDEVEAEAKESGPTTYKVTSTLTIKESDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAEDRIIKEEEARL-----SGRD---MOVTSOPVIAELPPKVSVFVPPRDGFFGNPRKS
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Ig mu chain C region (allele b) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: A24976
R;Schreiter, P.H.; Quester, S.; Bothwell, A.
Nucleic Acids Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag cisuserfamily: immunoglobulin C region; immunoglobulin homology C;Superfamily: immunoglobulin C region; immunoglobulin homology cimulation; glycoprotein; heterotetramer; immunoglobulin F;16-77/Domain: immunoglobulin homology cimulation; p;115-183/Domain: immunoglobulin homology cimulation; p;115-183/Domain: immunoglobulin homology cimulation; p;220-288/Domain: immunoglobulin homology cimulation; p;230-396/Domain: immunoglobulin homology cimulation; p;330-396/Domain: immunoglobulin homology cimulation; p;330-396/Domain: immunoglobulin homology cimulation; p;330-396/Domain: immunoglobulin ho
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A;Accession: A02145
A;Molecule ****
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A; Residues: 1-423 <ISH>
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C;Accession: A02145
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A;Molecule type: DNA
A;Residues: 1-455 <KAM>
A;Cross-references: GB.J00443
A;Cross-references: GB.J00443
A;Note: the sequence was determined from the germline gene
R;Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R.
Gene 15, 33-42, 1981
A;Title: Sequence of the gene for the constant region of the la.Reference number: A26239; MUID:82051295; PMID:6795090
A;Accession: A26239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382
A;Experimental source: strain C57BL/6
A;Note: the authors translated the codon AAG for residue 65 as Leu
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
R;Auffray, c., 77-86,
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                                 A; Note: the sequence was determined from the R; Auffray, C.; Rougeon, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-455 <SCH>
                                                                                       A;Residues: 1-455 <GOL>
                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A02166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAREQUALRESATVICLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST-----DIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPP----GSSP---SVQCR----SPR-----GKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNKDLHVPIPAVAEMNPNVNVF
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                                                                                                                                                                                                   of Balb/c
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F;129-201/Domain: immunoglobulin homology <IVM2>
F;239-307/Domain: immunoglobulin homology <IVM3>
F;346-417/Domain: immunoglobulin homology <IVM3>
F;346-417/Domain: immunoglobulin homology <IVM4>
F;446-455/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89/Disulfide bonds: #status experimental
F;26-89/Disulfide bonds: #status experimental
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (covalent) #status
F;16-199,246-305,353-415/Disulfide bonds: #status predicted
F;216,454/Disulfide bonds: interchain (to heavy chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455 <KEH>
C;Genetics:
A;Introns: 1/1; 106/1; 219/1; 325/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology c;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin, homology c;Mills
C;Superfamily: immunoglobulin homology c;Mills
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A; Residues: 1-225, 'N', 227-257, 'S', 259-367, 'K', 369-455 < AUF;
R; Kehry, M.; Sibley, C.; Fuhrman, J.; Schilling, J.; Hood,
Proc. Natl. Acad. Sci. U.S.A. 76, 2932-2936, 1979
A; Reference number: A26241; MUID: 79223904; PMID: 111247
A; Contents: annotation; MOPC 104E
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R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; S
Biochemistry 21, 5415-5424, 1992
A;Title: Complete amino acid sequence of a mouse mu chain: h
A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Contents: MOPC 104E
A;Accession: B02039
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A;Contents: TEPC183
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Best Local S
Matches 116
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398
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                                        SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                      GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                                                                   --TFTIPPSFAD-IFLSKSANUTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                   PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                   YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPP----GSSP---SVQCR----SPR------GKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSOVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF
SILTVTEEEWNSGETYTCVVGHEALPHLVTERTVDKSTG
                                                                                                                                        PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                        VKGFSPADÍSVQWLQRGQLLPQEKÝVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 362; DB 1;
Pred. No. 7.2e-15;
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R;Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon
A;Reference number: I36948; MUID:87147196; PMID:3103123
A;Accession: I36948
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A;Cross-references: GB:J00222; NID:g184755 R;Zhang, K.; Saxon, A.; Max, E.E.
                                                                                                                        R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T
EMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human
A;Reference number: A23195; MUID:84207910; PMID:6327276
                                                                                                                                                                                                 A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-428 < FLA>
                                                                                                                                                                                                                                                                                                                            A; Title: The sequence of a human immunoglobulin epsilon A; Reference number: A22771; MUID:84236029; PMID:6234164
                                                                                                                                                                                                                                                                                                                                                                              R;Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                             Ig epsilon chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 103/1; 209/1; 317/1 C; Superfamily: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-426 < RES>
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
                                                    A;Residues: 2-428 <UED>
                                                                           A; Molecule type: DNA
                                                                                                     A; Accession: A23195
                                                                                                                                                                                                                                                                                                  A; Accession: A22771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
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Pred. No. 7.2e-15;
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-358,'L',360-428 <MAX>
A;Residues: 1-358,'L',360-428 <MAX>
A;Cross-references: GB:J00222; NID:g184755
A;Onte: this sequence difference may be due to polymorphism
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments,
A;Reference number: A94418
A;Accession: A94418
                                                                                                                                                                          A;Status: preliminary; not compared with conceptual translati
A;Molecule type: mRNA
A;Residues: 382-426 <HEL>
A;Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1;
A;Experimental source: B cell myeloma U-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A;Experimental source: myeloma protein Nd
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A;Reference number: A33933; MUID:83065234; PMID:6815656
A;Accession: B93933
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A;Residues: 320-428 <ZHA>
A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
A;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.;
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloning and nucleotide sequencing of A;Reference number: A93491; MUID:83168897; PMID:8300763
                           A; Molecule type: mRNA
A; Residues: 382-391 <
                                                                                                                                                                                                                                                                                                                                Bur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and a A;Reference number: A46536; MUID:93122085; PMID:8419166
A;Accession: C46536
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A;Title: Purification and characterization
A;Reference number: S02438; MUID:88083554;
A;Accession: S02438
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A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: GB:L00022; NID:gli
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A;Title: Duplication and deletion in the human immunoglobulin epsilon

A;Reference number: A90824; MUID:83001945; PMID:6288268
                                                                                   A;Status: preliminary; not
                                                                                                                         A; Accession: D46536
                                                                                                                                                  A; Note: sequence extracted
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GB:S55276; NID:g263168;
                                  <HE2>
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forms of human immunoglobulin E encoded by alternative RNA splicing
PH1214; MUID:92308839; PMID:1613458
                                                                                                                                                        from
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                                                                                       compared with conceptual translation
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                                                                                                                                                     NCBI backbone (NCBIP:125297
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   PIDN:AAB24858.1; PID:g263169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human IgE
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                                                                                                                                                                                                             PID:g263167
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EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited A;Reference number: S00390; MUID:88283642; PMID:3135182
A;Accession: S00390

R; Parvari, R.; Avivi, A.;

Lentner,

Ή . . Ziv,

E.; Tel-Or, S.;

Burstein, gene

Y.; Schechter,

¥

repertoire,

combinato H

Accession: S00390

70

A;Cross-references: EMBL:X07174
A;Note: this sequence was determined from C;Superfamily: immunoglobulin C region; ir

immunoglobulin homology

differentiated

the

A; Molecule type: mRNA A; Residues: 1-504 < PAR >

Ig gamma chain (clone 36) - chicken (fragment)
N;Alternate names: Ig nu chain
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000

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A;Cross-references: GDB:11935; OMIM:147180
A;Map position: 14932.33-14932.33
A;Introns: 1/1; 104/1; 2:1/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into law C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology c;Mapping c;M
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F;232-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM3>
F;134/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:123483)
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A;Note: sequence extracted from NCBI backbone (NCBIP:125299)
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Best Local
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GKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEP
                                                                                  PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                                                                                                             PRAAPEVYAFATPEWPGSRDKRT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTT
                                                                                                                                                                                                                                                           QPREPQVYTL----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DSTKKCADSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS
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28.9%;
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Pred. No. 7.2e-15;
3; Mismatches 137;
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F;130-202/Domain: immunoglobulin homology <IMM2>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;249-420/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted
F;28-90,137-200,249-308,356-418/Disulfide bonds: (Abn) (covalent) #status predicted
F;419,457/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molocule type: mRNA
A; Residues: 1-458 <BER>
A; Residues: 1-458 <BER>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin proposition; immunoglobulin homology <IMM1;
E; 21-92/Domain: immunoglobulin homology <IMM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete Bequence of a cloned cDNA encoding rabbit A;Reference number: A02164; MUID:84088930; PMID:6418803 A;Contents: a2 allotype A;Accession: A02164
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                                                                                                                                                                                    AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
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                                                             ----SSRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
                                                                                                                                             ALTDGNLVAMG-----CLARDFLPSSVTFSWSFKNNSEI--
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                        14.9%; Score 360; DB 1;
23.8%; Pred. No. 9.6e-15;
tive 76; Mismatches 145
                                                                                                   -IEDSDTY-ICEVEDQKEEVQLL
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                                                                                                                                                                                                                                                              Length 458;
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                                                                                                                                                                                                                            156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of V-Ha2
                                                                                                                                                                                                                                                                                                                                              predict
                                                           A;Title: Nucleotide sequence of Suncus murinus immunoglobulin A;Reference number: S03961; MUID:89232144; PMID:2497033 A;Accession: S03961
                                                                                                                                                                           Ig mu chain C region - house shrew (fragment)
C;Species: Suncus murinus (house shrew)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
                     A; Molecule type: DNA
A; Residues: 1-457 <ISH>
                                                                                                                      C;Accession: S03961
R;Ishiguro, H.; Ichihara, Y.;
FEBS Lett. 247, 317-322, 1989
                                                                                                                                                                                                                                                                                                                                                               Ś
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-71 < RES>
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  A;Cross-references: EMBL:X13920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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CD4 receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vopr. Virusel. 40, 100-102, 1995
A;Title: [Nucleotide sequence of two exons of the human T-lymphocyte CD4 receptor gene]
A;Reference number: 160082; MUID:95407135; PMID:7676667
A;Accession: 160082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: I60082
R;Zverev, V.V.; Sidorov, A.V.; Nedospasov, S.A.; Maliushova, V.V.; Udalova,
                                             ILGNQGSFLTK 71
                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSTQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
ILGNOGSFLTK 71
                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVFVQWQQRGQPLSSDKYVTSAPAPEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFTCTVTHADLPFPLKHTISKSREVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTDLTTYG-SLNISW-----ASHNGKALDTHMNITESHPNATFSAMGEASVCAEDWESGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPHMVTERTVDKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFDKNVSMSSECSTTPSP------GIQVFPIAPSFADT-FLSKSARLICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GKNI QGG-----
                                                                                                                                                                                                                                                                                                                                                  T-cell surface glycoprotein CD4; immunoglobulin homology
                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                               14.8%;
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                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                 Score 357; DB 2;
Pred. No. 1.7e-15;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                        Length
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Y.; Namikawa,

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Nagatsu, T.; Kurosawa,

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A; Map position: (C; Superfamily: ir C; Keywords: immul F; 234-305/Domain
                                                                                                                                                                                                                                                                                                                                                                                                   Ig mu chain C region - rat (name rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
C;Accession: S25644
C;Accession: S25644
T.: Soulillou, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G:Genetics:
A;Introns: 106/1; 221/1; 327/1
A;Introns: 106/1; 221/1; 327/1
C;Superfamily: immunoglobulin C region; immunoglobulin
C;Keywords: immunoglobulin
F;241-309/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-343 < PAR>
                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S25644
A; Accession: S25644
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submitted to the EMBL Data
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                                                                                                                                                                                                  234-305/Domain:
                                                                                                                             Matches
                                                                                                                                                                                                                     Keywords: immunoglobulin
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Best Local
                                                                                                                                              Local
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to the EMBL Data Library, September 1992
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                                                                                                                                              Similarity
                KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                      TVEAKGSRPQTYKVISTLTITESDWLNLNVFTCRV--DHRGLTFWKNVSSTCAASPST--
                                                                                       SVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYVTSNPTPEPQNPGLYFVHSILTVSEKDWSSGESFSCVVGHEALPLSVTEKAVDKTSG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSLSRPKDVANDPPSVFVLPPAQEQLKLRESASITCLVKDFSPPDVFVQWQHHGQPVDPK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTISKAKGQPRE-PQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISWSRQNGEALQTHVNISESHPNSTFTAKGHASVCREEWESGEKFTCTVQHSDLPSPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPRTIVMSWLQRGEPVQPSLVSTSAVEAEPKGSGPTTFRVISRLTITENEWLSQREFTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTYI-CEVEDQKEEVQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPDETQ------VTLGCLARDFLPRPVTFSWKFKNSSSI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPAATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALHKGLTFOKNVSSVCMGDDTSTGISVFLLPPTFAN-IFLTQSAQLTCLVTGLATYD-SL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SSQNIY---NFPEVFTGGKYMATSQVLLPSTAILQSTDDYITCHTKHTTGEKEKK
                                                                                                                                                                                                                                  immunoglobulin C
                                                                                                                             Conservative
                                                                                                                                                                                                immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                         EMBL:X68312;
                                                                                                                                                                                                                                                                                        spleen
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25.5%; Pred
71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LG-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
                                                                                                                                            14.6%; Score 353; DB 2; 30.0%; Pred. No. 1.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ELQVTPELPPNVSIFV---PPR--NSFSGNHPRTSQLICQASGF
                                                                                                                             66;
                                                                                                                                                                                                                                    region;
                                                                                                                                                                                                                                                                                                         NID:g56461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 354.5; DB 2;
Pred. No. 2.1e-14;
'1; Mismatches 163;
Mismatches
                                                                                                                                                                                                                                    immunoglobulin
                                                                                                                                                                                                                                                                                                         PIDN: CAA48392.1;
                                                                                                                           107;
                                                                                                                                                           Length
                                                                                                                         Indels
                                                                                                                                                                                                                                    homology
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A;Introns: 105/3; 218/3; 324/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into late C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Copy of Mania: immunoglobulin homology cIMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;128-200/Domain: immunoglobulin homology <IMM2>
F;238-306/Domain: immunoglobulin homology <IMM3>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;45,112,139,192,210,238,257,280,326,441/Binding site:
F;135-198,245-304,352-414/Disulfide bonds: #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-454 <MCG>
A;Note: the sequence was determined from A;Note: the authors translated the codon C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 13, 5611-5628, 1985
A;Title: Phylogenetic conservation of immunoglobulin heavy
A;Reference number: A02168; MUID:85297761; PMID:2994005
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      74
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Mesocricetus auratus (golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A02168
PSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGS--FFLY 392
                                                                      SHPNGTFSAIGEANVCVEDWDSGKEFVCTVTHRDLPSPQKKFISKPRGMNKTPPAVYQQP
                                                                                                                                                                                                         LGGPSVFLFPPKPKDT-LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
                                                                                                                                                                                                                                                      PRTYKVISTLTITESDWLNLSVYTCRV--DHRGLTFWKNVSSTCAASPST-----
                                                                                                                                                                                                                                                                                                                                               SVFVPSRDAFSGPAPRKSRLFCEASNFSPKQITVSWLRDGKPVKSGFTTEPVTPEDRGSG
                                                                                                                                                                                                                                                                                                                                                                                           SPSVQCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      P---PKSVLEGSDEYLVCKVHHGNTNKDLRVPIPGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAMGCLARDFLPSSISFSWNYQNKSEV--NQGVRTFPTL-----RMGEKYAATSQVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VELTCTASQ--KKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNTKIMESHPNGTFSAVGVASVCMEDWDNRKEFVCTVTHRDLPSPQKKFISK----PNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE- 330
                                                                                                                EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR-EPQVYTLP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLIIKNLKIEDSDTY-ICEVE--DQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
                                                                                                                                                               ----DIQAFPIPPSFVGIFLNKSATLTCLVTNLATYD-TLNISWSSRSGEPLETKTKLTE 276
                                                                                                                                                                                                                                                                                              -----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DILAFP----IPPSFAD-IFLTKSAKLSCLVTNLATYD-TLNISWSSKSGEPLE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.R.; Tucker, P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.5%; Score 349; DB 1;
24.6%; Pred. No. 4.5e-14;
tive 82; Mismatches 154
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                                                                                                                                                                                                                                                                                                                                                                                         SPR-----GKNIQGG-----
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GGT for residues 105 and 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 454;
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Ig gamma-2a chain C region (E5.7A12) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_c C;Accession: B30503 R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K. J. Immunol. 141, 1754-1761, 1988 A;Title: DNA rearrangements affecting both variable and co A;Reference number: A30503; MUID:88315788; PMID:2842402 A;Accession: B30503 A;Molecule type: mRNA A;Residues: 1-112 <GIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 76
C31933
Ig mu chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1990 #sequence_revision 30-Jun-1992 #text_cha
C;Accession: C31933
R;Schwager, J; Mikoryak, C.A.; Steiner, L.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
A;Title: Amino acid sequence of heavy chain from Xenopus lae
A;Reference number: A94192; MUID:88176921; PMID:2451244
A;Accession: C31933
A;Molecule type: mRNA
A;Residues: 1-453 «SCH»
C;Superfamily: immunoglobulin C region; immunoglobulin homol
C;Keywords: immunoglobulin
                                                                                                                                                                                                           RESULT
B30503
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Matches 119
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                                                                                                                                                                                                                                                                                                                                                                               LVKGFYPSDIAVEW--ESNGQPENNYKTTP-----PVLDSDGSFFLYSKLTVDKSRWQQ
                                                                                                                                                                                                                                                                                                                     GNVFSCSVMHEALHNHYTQKSLSLSPG-----LQLDETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCLATNFTPTHI-----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVWD--NIEQFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                     CADEWNNDK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISRTPEVTCVVDDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTLYSCVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQ------LLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GESMDPVTIGCLAKDFLPETISFTWGDKNNASYSTGLKSYKPVMQSSGTYSASSQVNVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSF----LTKGPSKLNDRADSRR
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                                                                                                                                                                                                                                                                                  GDSFSCVVGHESLPLQLTQRSIDKSSGKPTNVNVSLVLSDTC
                                                                                                                                                                                                                                                                                                                                                              LVKGFSPSE1FVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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Pred. No. 7.3e-14;
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A;Cross-references: GB:M21925
A;Experimental source: myeloma cel
A;Note: the authors translated the
C;Genetics:
A;Introns: 100/3
C;Superfamily: immunoglobulin C re
C;Keywords: immunoglobulin
F;1-70/Domain: immunoglobulin home
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A; Residues: 1-577 < VAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Vazquez, M.; Mizuki, N.; Flajnik, M.F.; McKinney, E.C.; Kasmol. Immunol. 29, 1157-1158, 1992
A; Title: Nucleotide sequence of a nurse shark immunoglobulin A; Reference number: 150731; MUID:92357056; PMID:1495502
A; Accession: 150731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
C;Accession: I50731
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                             VLQNQKKVEFKIDIVP-CPA-
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                                                             CEVRHSGSDKSTGMPCPDGFPTALLTVSSSEEIESRKFAIIVCSISDFHSKSISVTW---
                                                                                            -ELQDSG----
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-LKNGRSVDSGIFTSPVCEANGNFSVTSRLRVPYAEWFDRAVYTCQVKYKEVIQSWNITG
                                                                                                                          GCLAMDYSPDVASVTWKKHGQLITTGVQTYPSVRNKKGTYTLS-SQLALIESDAECDQIS
                                                                                                                                                                                         ----TRRMSGYEYLGGHSGYWGQGTMVTVTTATP--SSPTLYGLVSSCQQGNIDGSVIY 168
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llarity 24.3%;
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%; Pred. No. 1.6e
83; Mismatches
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                            PEPKSCDK-THTC----PEL----LGG
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A;Accession: S31436
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C;Species: Ambystoma mexicanum (axolotl)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A; Residues: 1-433 < FEL>
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R;Fellah, J.S.; Wiles, M.V.; Schwager, J.; Charlemagne, submitted to the EMBL Data Library, November 1992
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;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                LDSD----GSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 417
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QEAGTAGLGTYFSYSMLTIQKSDWDKRETFTCVAAHSAV
                                                                                            GQPREPQVYTLPPSRDELTK-NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPV
                                                                                                                                              EGPEEAAVISEQYIDSDGTFTAMSYLNITKNEWERGDEFTCKVKHFDLPFPLSRSVSKPT
                                                                                                                                                                                  TKPRE----EQY---NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                                       CADSQTPYQPKVFLIAPKARD-LYTANQPVVICKITKMENSD-SLSVTW------KRR
                                                                                                                                                                                                                                                         CPELLG--GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                QKDGQGTFSTTSQINVTKSDWASGDKYTC-----KVEH-----PATSSRAEDTIHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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24.2%; Pred. No. 2e-
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RESULT

80

G. W

Ig mu chain (C;Species: HC;Date: 30-Ju A;Cross-references: EMBL:X07784; NID:g63963; PIDN:CAA30617.1; PID:g63964
A;NOte: the sequence was determined from the differentiated gene
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IMI>
F;20-87/Domain: immunoglobulin homology <IMI

F;20-87/Domain: immunoglobulin homology <IMI R;Wilson, M.R.; van Ravenstein, E.; Miller, N.W.; Clem, L.W.; Middleton, D.L.; Dev. Comp. Immunol. 19, 153-164, 1995
A;Title: cDNA sequences and organization of IgM heavy chain genes in two holost A;Reference number: I50006; MUID:96039719; PMID:7556802 Ig mu chain - Lepisosteus osseus (fragment)
C;Species: Lepisosteus osseus
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 03-Nov-2000
C;Accession: I50830 F;123-190/Domain: immunoglobulin homology <IM2>
F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;366,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn) EMBO J. 7, 1979-1988, 1988
A;Title: Complete structure and organization of immunoglobulin heavy
A;Reference number: S00980; MUID:88328985; PMID:3138109
A;Accession: S00980 δ 밁 ঠ g S 밁 S 밁 Ş B Ś 밁 á 뮍 Ś A; Molecule type: mRNA A; Residues: 1-438 < KOK> A;Accession: I50830 ;Accession: S00980; K.; Litman, R.; Shamblott, M.J.; Litman, g mu chain C region (clone 12022) - horn shark (fragment) ;Species: Heterodontus francisci (horn shark) ;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 Query Match Best Local : Matches 81 Match 12.9%; Local Similarity 25.4%; 395 407 335 350 183 179 127 275 292 227 237 113; 87 49 23 SYSCVVGHEAIPLKIINRTVNKSSG VFSCSVMHEALHNHYTQKSLSLSPG 431 LTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSDG-SFFLYSKLTVDKSRWQQGN NISTQAWLSGAEFYCVVSHQDLPTPLRASIHKEEVKDLREPFVSVLLPPAEDVSAQRFLS TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVS MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVVSVL 291 NTVYTCQVAHQEVTQSRNITGSQVPCS------IGDPVIKLLPPSIEQVL SGTWTCTVLQNQKKVEFKI--DIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTL TVLCSIIDFHPESITVSWLKDGQPMDSGFVTSPTCEVNG----NFSATSRLTVPAGEWFS 182 VRRGESLW------ADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL-----TTGLKIYPSVLNKKGT------YTRSSQLTITESE-----VGSSKIYCE TQGNKV----VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDR LTCLVRGFSPREIFIKWTVNDKSVNPGNYKNTEVMAENDNRSFFIYSLLSIAAEEWASGA -LEATVTLTCV---VSNAPYGVNVSW-----TQEKKPLKSEIAVQPGEDSDSVISTV -----LQGQSLTLT-----LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQD Conservative ; Score 312; DB 1; 1; Pred. No. 7.7e-12; 67; Mismatches 155; ----IKEILDCKGDIVPPTVILTQSSSEEITSRRFA 126 419 Length 438; Indels 110; ଜ.₩. (covalent) #status Gaps two holostean fish. chain constant regio 349 274 226 133 86 79 334 236 17 Warr,

gre

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RESULT 82

S21461

T-cell surface glycoprotein CD4 (allele 1) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Ante: 20-Feb-1995 #sequence revision 19-Apr-1996 #text_change
C;Accession: 147131; S21461
R;Gustafsson, K.; Germana, S.; Sundt, T.M.
J. Immunol. 151, 1365-1370, 1993
A;Title: Extensive allelic polymorphism in the CDR2-like region
A;Reference number: 147131; MUID:93329116; PMID:8335933
A;Accession: 147131
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                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 - GUZ>
A;Cross-references: EMBL:X65629; NID:g1928; PIDN:CAA46583.1; PID:g388232
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: glycoprotein, T-cell
F;3-81/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-474 <WIL>
A;Cross-references: EMBL:U12455; NID:g529949; PIDN:AAC59688.1; PID:g529950
C;Genetics:
A;Gene: IgM
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Best Local S
Matches 59
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Best Local
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                                                                                                                                       Similarity
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NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN 128
                                       KAGDLAELPCHSSQKKNLPFNWKNSNQTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG
                                                                KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG
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                                                                                                                    Conservative
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                                                                                                                12.7%; Score 305.5; 60.2%; Pred. No. 3.4e tive 16; Mismatches
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                                                                                                                                     .4e-12;
                                                                                                                                                         DB 2;
                                                                                                                  22;
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novel antigen receptor precursor - nurse shark C;Species: Ginglymostcoma cirratum (nurse shark) C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change C;Accession: S60266
R;Greenberg, A.S.; Avila, D.; Hughes, M.; Hughes, A.; McKinney, Nature 374, 168-173, 1995
A;Title: A new antigen receptor gene family that undergoes rearr A;Reference number: S60266; MUID:95183140; PMID:7877689
A;Accession: S60266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Immunol. 149, 855-861, 1992
A;Title: Chicken IgA H chains. Implications
A;Reference number: A46507; MUID:92340889; F
A;Accession: A46507
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A;Residues: 1-585 <MAN>
A;Residues: 1-585 <MAN>
A;Cross-references: GB:S40610; NID:g251907; PID:g251908
A;Cross-references: cnconsistent with the nucleotide translation
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:109906, NCBC)Superfamily: immunoglobulin C region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig alpha chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 18-Jun-1993 #sequence_revi
C;Accession: A46507
R;Mansikka, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A46507
A;Status: preliminary; nucleic
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Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                             DKNAG
                                                                                                                                                                                                                                                                                                                      SLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                              GQP--ENNYKTTPPVLDSDGSFF-LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                       GV-VVAEESIRKETDTPLHAPSVYVFPPPPAEELSLQETATLTCMASSFLPSSILLTWTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPAPIEKTISKAKGQP-REPOVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-GVSVSWSRSSGGGLDV----SQTEDRQADGRYTVRSFLRVCAEEWNGGETFGCSVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPEVKFNWYVD---GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNEEMT----PAPESDESGCSDCTESGVTQWSRVNVTRKSWEGGAQFGCRVTHGALK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVE
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    acid
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  sequence not
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PMID:1634774
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                                                                                                E.C.; Flajnik,
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                                                                                                                                       21-Jul-2000
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47175
R;Brown, W.R.; Butler, J.E.
Mol. Immunol. 31, 633-642, 1994
Mol. Characterization of a C alpha gene of swine.
A;Reference number: I47175; MUID:94254897; PMID:7545929
A;Accession: I47175
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C;Superfamily: im
F;232-304/Domain:
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C;Genetics:
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A; Residues: 1-342 < BRO>
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Best Local S
Matches 96
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                                   QDSGTWTCTVLQNQKKVEFKIDIVFCPAPEPKSCDKTH-----TCPE
                                                                  LTLGSSEPAGYVVIACLVRDFFPSEPLTVTWSPSREGVIVRNFPPAQAGGLYTMSSQLTL
                                                                                                   LTLTLESPPG-----SSPSVQCRSPRGKNI-----QGGKTLSVSQLEL
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                                                                                                                                                                                                                       immunoglobulin C region; immunoglobulin homology
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                                                                                                                                       Conservative
                                                                                                                                                                                                         immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                        EMBL: U12594; NID: g555826; PIDN: AAA65943.1;
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25.1%; Pred. No. 5.6e-11;
                                                                                                                                     12.4%; Score 300; DB:
27.1%; Pred. No. 3.1e-
live 44; Mismatches
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----PVEQCPADQILKCQVQHLSKSSQSVNVPCKVLPSDPCPQ
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A;Molecule type: DNA
A;Residues: 1-339 <BUR>
C;Superfamily: immunoglobulin C region; immunog
C;Keywords: immunoglobulin
F;124-190/Domain: immunoglobulin homology <IMM>
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A;Actaus: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig alpha chain C region - rabbit (fragment)
C;Species: Orycrolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
DWNQGDSYSCVVGHEGLAEHFTQKTIDRQAG
                                                                                                             Q-VSLTCLVKGFYPSDIAVEWESNG--QPENNY---KTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                  LQNQKKVEF-----KID---IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLY
                                    RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                               ALVTLTCLVRGFSPKDVLVYWTNKGVVVPKDSFLVWKPLPEPGQEPTTYAVTSLLRVSAE
                                                                                                                                                        SSVLPGCAETWTAGTEFTCTVTHPEIEGSSLTATIRKDTGSLTPPQVHLLPPPSEELALN
                                                                                                                                                                                            VSVLTVLHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                   LRD-LLLGSDASLTCTLRGL--KDPKDAVFTW-----EPTNGNEPVQQSPQRDPCGCYSV 169
                                                                                                                                                                                                                                                                     PKDTLMISRTPEVTCVVVDVSHEDP-EVKFNWYVDGVEVHNAKTKPREEQYN---STYRV 287
                                                                                                                                                                                                                                                                                                                                                                                         LSLPCPLSGQPVVV-----GCLIQGFFPLGPLNVKWTISGENVTFPPVQLDTSGLYTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLRVDAEDWKQGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEELALNELVTLTCLVRGFSPKDVLVRWLQGGQELPRDKYLVWESLPEPGQAIPTYAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSC-GCYSVSSILPGCADPWNKGETFSCTAAHSELKSALTATITKPKVNTFRPQVHLLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC-KPSLSLQPPALAD-LLLGSNASLTCTLSGLKKSE-GVSFTWQPSGGK-DAVQASPTR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
                                                                                                                                                                                                                                                                                                                LLNLTDEECPTCVACHVEHNEVDRYLILPCP-----DTHSSCPPTSCGEPSLSLQRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG----LQLDETCAEAQ 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 297; DB 2;
Pred. No. 4.7e-11;
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320
                                      431
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Ig alpha chain C region - rabbit (fragment) (Species: Oryctclagus cuniculus (domestic rabbit) C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 (c;Accession: S0926) (c;Accession: S0926) (c; Hanly, W.C.; Zhai, S.K.; Knight, K.; Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K. EMBO J. 8, 4041-4047, 1989 A;Title: The IgA heavy-chain gene family in rabbit:

family in rabbit: cloning

and

sequence analysis

of 13

Χ.L.

#text_change 16-Jul-1999

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F;151-219/Domain: immunoglobulin homology <IMM3>
F;258-329/Domain: immunoglobulin homology <IMM4>
F;358-329/Domain: carboxyl-terminal <CTS>
F;347-367/Domain: carboxyl-terminal <CTS>
F;551,119,303,354/Blnding site: carbohydrate (Asn) (covalent) #status predicted
F;56-111,158-217,265-327/Disulfide bonds: #status predicted
F;126,366/Disulfide bonds: interchain (to heavy chain) #status predicted
F;205/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-367 cDAH>
A; Residues: 1-367 cDAH>
A; Residues: 1-367 cDAH>
A; Cross-references: GB: K00389; NID: g212204; PIDN: AAA48923.1; PID: g212205
A; Cross-references: GB: K00389; NID: g212204; PIDN: AAA48923.1; PID: g212205
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin credion; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C; Keywords: immunoglobulin homology < IMM2>
E; 149-133/Domain: immunoglobulin homology < IMM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
MHCH
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A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-357 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin P;142-208/Domain: immunoglobulin homology <IVM>
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                                   ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 22-Jun-1999 C;Accession: A02170 R;Dahan, A.; Reynaud, C.A.; Weill, J.C. Nucleic Acids Res. 11, 5381-5389, 1983 A;Title: Nucleotide sequence of the constant region of a chicken mu heavy chain immunogl A;Reference number: A02170; MUID:83299221; PMID:6310496 A;Accession: A02170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig mu chain C region - chicken (fragment)
C;Species: Gallus gallus (chicken)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 VTVPSPP-----ECQPPTP-------GPSDTTTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                        GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCPCPSP-SC------GEPSLSLQRPFLRD-LLLNSNASLTCTLRGLKNPEGAV-F
  GPEVVAESRISVTESEWDTGATFSCVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLTAKISKDTGAIIPPQVHLLPPPSEELALNELVTLTCLVRGFSPKDVLVYWTNKGVNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG--QP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TW-----EPTNG-NKPVQQSVQSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQNESYTCVVGHEGLAEHFTQRTIDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNS----TYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-A 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                                                    12.3%;
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29.8%; Pred. No. 5.7e-11;
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0; Mismatches
                                                                                                         Score 296;
Pred. No. 5
                                                                                    Mismatches
                                                                                                           ຫ
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                                                                                                                          Length 367
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- EGEMRINTS KRMECGLE
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129
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A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIP:115354) C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Immunol. 22, 2595-2601, 1992
A;Title: Evolution of vertebrate IgM: complete amino acid sequence of the constant regio
A;Reference number: A46532; MUID:93011455; PMID:1382992
A;Accession: A46532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig mu chain C region - axolotl (fragment)
C;Species: Ambystoma mexicanum (axolotl)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: nucleic acid
A; Residues: 1-454 < FEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A46532
R;Fellah, J.S.; Wiles, M.V.; Charlemagne, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 111; Conserv
376 VNTKOAEEVDPTTGQKSCFMYSMLKIPAAQWTAGNTYTCVVGHEALPLQITQKSIDRSFG
                                                                                                                                                             321
                                                                                                                                                                                                                  266
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                                                                                                                                                       ISKAKG-QPREPOVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNY
                                                                                                                                                                                                                  KTEITNPIFHD.
                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                          KTHTCPELLGGPSVFLFPPKPK-DTLMISRTPEVTCVVVDV-----SHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                           GKDVTSG--IYTEEPVADTAGNFDVTSLLNIEPMDWNMDTVYSCVVDQTASKFWNTRNMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV-PCPAPE-----PKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLLQGQSLTLTLESPPG--SSPSVQCRSP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAOAPSVYPLISCGASLDPVVIGCLAKGFLPDSVTFDWTDKNNASFSAGVAKLPSVTTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATQGNKVV----LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKI---LGNQGSFLTK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVY 334
                                                 KTTPPVLDSD-----GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                      LOKPNGNORRKPSVYIYPPPSEELALKETATIVCLMRGYHPCDLFVRWLENSQQLQKQDY
                                                                                                                                                                                                                                                                                                                     KSMLCDAQVGPVKVTAFTVAPTFEDMFESKSANVTCIVTNMGTIEGFNITWSREDTNEVL
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Pred. No. 7
                                                                                                                                                                                                               NATLSVMGIATVCADQWDAHHKFVCKVLHQDLAEQRVLS
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'.5e-11;
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A;Cross-references: EMBL:X07781
A;Cross-references: EMBL:X07781
A;Note: the sequence was determined from the germline gene R;Kokubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, Proc. Natl. Acad. Sci. U.S.A. 84, 5868-5872, 1987
A;Title: Extensive families of constant region genes in a phyla, Reference number: A32716; MUID:87289703; PMID:3475706
                                                                                                                                                                                                                                                                                                                             A;Title: Complete structure and organization of immunoglobulin heavy chain constant reg. A;Reference number: S00980; MUID:88328985; PMID:3138109
A;Accession: S01854
                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Heterodontus francisci (horn shark) C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 C;Accession: S01854; C32716; Ā46530 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J EMBO J. 7, 1979-1988, 1988
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                                           A;Cross-references: GB:M17186
C;Genetics:
                                                                                        A; Molecule type: DNA
A; Residues: 1-99 < KO2>
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A; Residues: 1-343
C; Superfamily: in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120 A;Accession: S09272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
                                                                                                                                   A; Accession: C32716
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                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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Complex:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
An immunoglobulin heterotetramer subunit consists of two identical light (kap
                      100/1; 206/1; 309/1; 419/1; 459/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHCYCP-PTSC-----GEPSLSLQRPDIGDLLLESKA-SLTCTLSGL--KDPEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
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31.7%; Pred. No. 5.9
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                                                                                                                                                                                                                                                                                                                                                                                                                      M.J.; Litman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change 16-Aug-1996
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglo F;20-87/Domain: immunoglobulin homology <IMM1>
F;123-190/Domain: immunoglobulin homology <IMM2>
F;228-291/Domain: immunoglobulin homology <IMM3>
F;238-291/Domain: immunoglobulin homology <IMM3>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;438-458/Domain: transmembrane #status predicted <TMM3>
F;47-85,130-188,235-289,337-398/Disulfide bonds: #status predicted (Asn) (covalent) #status F;164,200,245,275,374,411,415,437/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                  A;Gene: GDB:IGHA2
A;Gene: GDB:IGHA2
A;Cross-references: GDB:119333; OMIM:147000
A;Map position: 14q32.33-14q32.33
A;Introns: 1/1 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin C;Superfamily: immunoglobulin C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                Ig alpha-2 chain C region (allotype A2m(1)) - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999 C;Accession: B22360 R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H. Cell 36, 681-688, 1984 Cell 36, 681-688, 1984 A;Title: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 A;Reference number: A94653; MUID:84130179; PMID:6421489 A;Accession: B2360
                                                                                                                                                                                                                                                                                                      A; Molecule type: I
A; Residues: 1-340
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 12.2%;
Similarity 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SISPGIQUETCABAQDGELDGLWTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRNITGSQVPC----SCN-----DPVIKLLPPSIEQVL-LEATVTLTCV---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDGQHMESGFVTSPT--C--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFFPREIFVKWTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNAPYGVNVSW----TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSGAEFYCVVNHQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKKDNEPITTG-----LKTYPSVLNKKGTYTQS-----SQLTITESEVGSSKIY-CEVR
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     Conservative
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                                                                                                                                                                                                                                                                                                      <FLA>
                       12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                         Score 294.5; DB 2;
Pred. No. 6.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 295.5; DB 1; Pred. No. 8.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EDQKEEVQLLVFG--LTANSDTHLLQGQSLTLT-- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ 197
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 157;
                                                                                                                                                   homology
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Gaps
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Indels

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A;Introns: 100/1; 206/1; 309/1 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k C;Complex: An immunoglobulin cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglo F;1-438/Domain: C region <CRE> F;20-87/Domain: immunoglobulin homology <IMI>
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                                                                                                                                                                                                                                                                                                                                                              F;123-190/Domain: immunoglobulin homology <IM2>
F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;364,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-438 <KOK>
A;Cross-references: EMBL:X07781
A;Note: the sequence was determ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;KOkubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. EMBO J. 7, 1979-1988, 1988
A;Title: Complete structure and organization of immunoglobulin heavy A;Reference number: S00980; MUID:88328985; PMID:3138109
A;Accession: S01853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig mu chain C region, secreted (clone 3050) - horn shark C;Species: Heterodontus francisci (horn shark) C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 C;Accession: S01853
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Best Local Similarity
Matches 115; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
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SRNITGSQVPC----
                                  KIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                     KDGQHMESGFVTSPT--C----GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ
                                                                                                          ----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF
                                                                                                                                            RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
                                                                                                                                                                                                                    WKKDNEPITTG-----LKTYPSVLNKKGTYTQS-----SQLTITESEVGSSKIY-CEVR
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SCN-----DPVIKLLPPSIEQVL-LEATVTLTCV---V
                                                                                                                                                                                                                                                                                           65; Mismatches 153;
                                                                                                                                                                                                                                                                                                            Score 294; DB 1;
Pred. No. 9.6e-11;
                                                                                                                                                                                 ---EDQKEEVQLLVFG--LTANSDTHLLQGQSLTLT---
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                                                                                                                                                                                                                                                                                                                               Length 438;
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237
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Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
C;Accession: S09276
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K
                                                                                                                                      RESULT
S09276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X00353; NID:g1575; PIDN:CAA25100.1; PID:g1576
C;Comment: This immunoglobulin belongs to the IgA-g subclass. It was isolated from a rab. C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin; plasma F;86-152/Domain: immunoglobulin homology <IM1>
F;189-261/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Knight, K.L.; Martens, C.L.; Stoklosa, C.M.; Schneiderman, Nucleic Acids Res. 12, 1657-1670, 1984
A;Title: Genes encoding alpha-heavy chains of rabbit IgA: cha A;Reference number: A02174; MUID:84144059; PMID:6322114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-299 < KNI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A02174
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985
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Best Local (
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                                                   #text_change 16-Jul-1999
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Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
C;Accession: S09266
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning and A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09266
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C;Keywords: immunoglobulin
F;241-314/Domain: immunoglobulin homology <IMM>
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C;Keywords: immunoglobulin
F;228-300/Domain: immunoglobulin homology <IMM>
       밁
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A; Residues: 1-352 <BUR>
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A; Residues: 1-338 < BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09276
                                                                                                                                                                                                                                                                                                                                                                               A;Status: not compared with
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Best Local
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92; Conserv
                                                                                                                                                                                                                                   Similarity
                                                                                                            IVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE- 257
       AVFTWNPTNGNEFVQQST
                                        VKFNWY-VDGVEVHNAKTKPREEQYN-STYRVVSVLTVLHQDWLNGKEYKCKVSNKALP- 314
                                                                                                                                               LSLTPEQCP-EDHNVVCRVEH--NYDEGQNLTVLYPECKDPNS---------
                                                                                                                                                                                LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAEHFTQRTIDRLAG
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29.2%; Pred. No. 9.4e-11;
ative 50; Mismatches 133;
                                                                                                                                                                                                               12.1%; Score 292; DB 2; Length 35
31.2%; Pred. No. 9.8e-11;
ative 41; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                             conceptual translation
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                                                                         -GEPSLSLORPDIGD-LLLESNASLTCTLSGL--KDPEG
       QSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEG
                                                                                                                                                                                                                                                  Length 352;
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Ig alpha chain C region - rabbit (fragment)
(;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
C;Accession: S09265
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, F
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#text

_change 16-Jul-1999

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Ig heavy chain precursor V region - ladyfish
C;Species: Elops saurus (ladyfish)
C;Ste: 20-Uul-1990 #sequence_revision 20-Uul-1990 #text_change 21-Jul-2000
C;Accession: A34891
R;Amemiya, C.T.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990
A;Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene A;Reference number: A34891; MUID:90138916; PMID:2105490
A;Accession: A34891
A,Status: preliminary
A,Molecule tros. mPNn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M26182; NID:g213134; PIDN:AAA49238.1; PID:g213135 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-568 < AME>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APIEKTISKAKGOPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                            QGGKTLSVSQLELQD-SGTWTCTVLQNQKKVE--FKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPKDSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQGDSYSCVVGHEGLAEHFTQRTID 329
PAŚDWDSGVVYŚCAVHHETVMESVVKTIVRTTDSVSKKPTTVŚLDLNVPQTC
                                         DKSRWQQGNVFSCSVMHEAL------HNHYTQKSLSLSPGLQLDETC
                                                                                          PA-EQRNLSTVTLICYAKDFYPEQVLISWLVDDQPVETDVPTTEVVKTEGTYSVFSQLTI
                                                                                                                                         PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                        GQFDE-QKMISKLLIDYEEWKNRTEYTCKVEHSDLPSPLRTSYRRECGGKWQSPTVFILA
                                                                                                                                                                                                                                 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLP 337
                                                                                                                                                                                                                                                                                                                                 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE--VHNAKTKPRE 278
                                                                                                                                                                                                                                                                                                                                                                             TASSFLQASESQWKRLDGTFTCQFIQEGEITEQTVKYSSAEC-SPEAQIDAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATFACLATD-----FYPKGHSFKWLRDGKEVT-----DGIATLTECQKKGDKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGDFKSKAEFKCTTELGGKKT-----PVVIPKPEPPKPPRQPVLSIMTPSQEELTLNK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGSFLTKGPSKLNDRADSRRSLWDQGNFPLII------
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                                                                                                                                                                                                                                                                                  ---ISPPTPEE-LFLQQTRTLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 290;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152;
                                                                                                                                                                                                                                                                                     --KITGDVDGVRNVTWEVGSEVRV
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  566
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RESULT
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A,TItle: The IgA heavy-chain gene family in rabbit: cloning A,Reference number: $09264; MUID:90076124; PMID:2512120
A,Accession: $09265
A,Status: not compared with conceptual translation
A,Molecule type: DNA
A,Residues: 1-357 cBUR>
C,Superfamily: immunoglobulin C region; immunoglobulin homolc; Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                              A;Introns: 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;230-302/Domain: immunoglobulin homology <IMMS
                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-340 <RES>
A;Cross-references: GB:S71043; NID:g546798; PIDN:AAB30803.1; PID:g546799
                                                                                                                                                                                                                                                                                                                                                         R;Chintalacharuvu, K.R.; Raines, M.; Morrison, S.L.
J. Immunol. 152, 5299-5304, 1994
A;Title: Divergence of human alpha-chain constant region
A;Reference number: 156230; MUID:94246170; PMID:8189047
A;Accession: 156230
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig alpha-2 chain - human (fragment)
c;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I56230
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                                                                                                                                  Query Match
Best Local Simi
Matches 102;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LQGQSLTL-TLESPPGS-------SPSVQCR---SPRGKNIQGGKTLSVS 172
                                169 LSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
                                                                                                122 VFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKT 168
 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GD-LLLNSNASLTCTLRGLLNPEGAV-FTW----EPTFGKEPVQQSPQLDHCGCYSVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE---QYNSTYRVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSGESVIFPPVPSPPSSLYTTYSLLRLPAEQCPEENSVACRVEHNNKGQDVTVPSPPACN 102
TTSSQLTLPATQCPDGKSVTCHVKHYTNSSQ---DVTVPCRVPPPPPC-----C----H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLTCLVRGFSPKDVLVSWTHNGTPVVPKDSYLVWKPLREPGQDPTTYAITSLLRVPAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLD---SDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTIEPPTTPTC-----GKPSLSLQRPDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLPGCAVLWNAGTEFTCTVTHPEIEGDSLTGTISKDTGSLIPPQVHLLPPPSEELALNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-
                                                                VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                  11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%; Score 289; DB 2; 28.2%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches 122;
                                                                                                                                   50; Mismatches 144;
                                                                                                                                                   Score 286.5; DB Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431
                                                                                                                                                                  DB 2;
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                                                                                                                                   Indels
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A;Molecule type: mRNA
A;Residues: 1-370 <KOK>
A;Cross-references: EMBL:X07783; NID:963962; PIDN:CAA30616.1; PID:9833624
A;Cross-references: EMBL:X07783; NID:963962; PIDN:CAA30616.1; PID:9833624
A;Note: the sequence was determined from the differentiated gene
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap:
C;Complex: An immunoglobulin some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin (fragment) cregion; heterotetramer; immunoglobulin
F;1-370/Domain: C region (fragment) cCRE-
F;662-332/Domain: immunoglobulin homology <IMM>
F;67-332/Domain: #status predicted
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A; Accession: S01851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Complete structure and organization of immunoglobulin A; Reference number: S00980; MUID:88328985; PMID:3138109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kokubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, EMBO J. 7, 1979-1988, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S01851
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C;Species: Heterodontus francisci (horn shark)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sim
Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Local Similarity 26.2%;
les 101; Conservative 5
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326 ASYSCVVGHEAIPLKIINRTVNKSSG
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                                                        NVFSCSVMHEALHNHYTOKSLSLSPG
                                                                                                                                                                                                                                            VDISTQAWLSEAVFYCVVSHQDLPTPLRDSIHKEAWKDLREPSVSVLLPPAEEISAERFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WFTNTVYTCQVSHQAATQSRNI----TGSPDSSECNH------PAIKLLPPSIEQV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQLLVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPSKLNDRADSRRSLW------DQGNFPLIIKNLKIEDSD-----TYICEVEDQKEE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLPPPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                       SLTCLVRGFSPREIFVKWTVNDKSVNPGNYKNTEVMAENDKSSFFIYSLLSIAAEEWASG
                                                                                                                                                                         SLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                                                    LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLPPSRDELTKNQ-V 348
                                                                                                                                                                                                                                                                                                                                                                L-LEATVTLTCV---VSNAPYGVNVSW-----TQEQKPLKSEIAVQPGEDPDSVIST
                                                                                                                                                                                                                                                                                                                                                                                                                         LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVVSV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SPACETNG----NFSATSRLTVPARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSKIYCEVRRGESLWIKEIPDCKGDIVHPTVILTQTSSEEITSSRFATVVCSIIDFHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Mismatches 155;
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Search completed: August 3, 2004, 13:14:55
Job time: 16:4339 secs

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Result
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Maximum Match 100%
Listing first 125 :
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Perfect score:
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        Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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    Q01862
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5 mus musculu
3 macaca mula
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0 oryctolagus
2 cavia porce
8 carcopithec
7 mus musculu
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1 rattus norv
9 rattus norv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINB=71064027; PubMed=4923144;

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MEDLINE=81208100; PubMed=7236608;
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 282
                                              181
                                  66
                                                                               al Similarity
246; Conser
                                                        0
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                 SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG
                 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
           GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                        PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
                                                                   PSVQCRSPRGKNIQGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                        PS00290;
                                                                               Conservative
                                                                                                                                                                                    180
193
193
198
202
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238
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130
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157
163
165
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                                                                                                                                                                                                                                                                                                                             144
250
180
330
97
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111
224
27
103
109
112
                                                                                                      $
                                                                                                                                                                                                                                                                                                                                                                                                                        IG MHC; 2.
                                                                                                     317
325
36106 MW;
                                                                                                                      333330164760564474731667
                                                                                                                                                                                                                                                                                                                             110
223
330
109
109
112
204
112
308
308
180
330
                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                 239
                                                                                    50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                              Score 1227.5; I
Pred. No. 1.1e-7
7; Mismatches
                                                                                                                                                                                                                                                                                                                                  N-LINKED
REMOVED F
                                                                                                                                                                                                                                                                                                                                                                                CH1.
HINGE.
CH2.
CH3.
                                                                                                                                                                                                                                                                                                                 K -> R (IN G1M(3) MARKER).
/FTId=VAR_003886.
D-> E (IN G1M(NON-1) MARKER)
                                                                                                                                                                                                                                                                                                      /FTId=VAR_003887.
L -> M (IN G1M(NON-1) MARKER)
                                                                                                                                                                                                                                                                                                /FTId=VAR_003888.
                                                                                                      3770EE106C2FA33D CRC64;
                                                                   -----KTLSVS------QLELQDSG----
                                                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONALLY
                                                                                                                                                                                                                                                                                                                                                                                                                  C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                         HTIW)
                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                         LIGHT
HEAVY
HEAVY
                                                                               Indels
                                                                                          Length 330;
                                                                                                                                                                                                                                                                                                                                                         CHAIN)
                                                                               55;
                                                                               Gaps
341
                                 119
                                                        65
           179
                       281
                                             221
                                                                    180
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RESULT 2
GCG -1-- I
CCC -1-- I
CCCC -1-- I
CCC -1-- I
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frangione B., Rosenwasser E., Prelli F., "Primary structure of human gamma 3 immun gamma 3 heavy-chain disease protein Wis." Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene deletion model.";

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has interchain disulfide bond at position 7 in addition normally present in the hinge region.

-!- MISCELLANEOUS: The heavy chain disease protein WIS interchain with the beavy chain disease protein with the beavy chai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Frangione B., Prelli F., Fra Wolfenstein-Todel C., Frangione B., Prelli F., Fra "The amino acid sequence of 'heavy chain disease' Structure of the Fc fragment of immunoglobulin G3. Biochem. Biophys. Res. Commun. 71:907-914 (1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human
quadruplication of a 15-amino acid residue basic u
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GC3_HUMAN
P01860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
MEDLINE=82247835; PubMed=6808505;
Alexander A., Steinmetz M., Barritault D., Frangi
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (DISEASE PROTEIN WIS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-MAR-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 59-289 (PROTEIN WIS/DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=81021548; PubMed=6774747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-3
IGHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 12-97 (PROTEIN WIS).
                                                                                            of the CH1 region, and part of the hinge compared with norm gamma-3 heavy chains.

MISCELLANGOUS: Disease protein OMM may represent an allelic or another gamma chain subclass.

MISCELLANGOUS: The hinge region in gamma-3 chains is about times as long as in other gamma chains and contains three identical 15-residue segments preceded by a similar 17-resi
                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: Disease protein WIS and all of the CH1 region.
MISCELLANEOUS: Disease protein ZUC
                                                                 segment (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01,
01,
43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The heavy chain disease protein WIS The sequence of residues 42-76 was t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
gion (Heavy chain disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin
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                                                                                                                                                                                                                                                                                            lack most of the V hinge compared with
                                                                                                                                                                                                                                                                                                                                                                                             is lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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unit.";
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                                                                                                                                                                                                                                     an allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taken from
                                                                                                                                                                                                                                                                                                                                                                                                   of the V region
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17-residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zuc.;
                                                                                                                                                                                                                                                                                                                                  region,
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the 11
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SWISS-PROT entry

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Best Local S
Matches 209
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00407; IGcl; 1.
                                                                                                                                                                                                                                              DISULFID
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MOD RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBI outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as sits content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   SEQUENCE
                                                                                                                                   VARIANT
                                                                                                                                                    VARIANT
                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                           Pyrrolidone
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00231; AAA52805.1; ALT_SEQ. HSSP; P01857; 1FC1.
                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                      VARĪANT
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147120;
                255
                                53
                                                                          Similarity
          DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
DPEVQFKWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALP
                                 PCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                         PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                   290
                                                                  Conservative
                                                                                                                                                                                                                     carboxylic acid.
                                                                                                                                                   227
                                                                                                                                                                    182
                                                                                                                                   227
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                                                                                                   Ā
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                                                                                                                                                                                                      134
                                                                                                   32331
                                                                         46.9%;
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¥
                                                                  13;
                                                                                                                                                            F -> Y \117

/FTId=VAR 003892.

T -> A (IN OMM).

T -> A (OMM).
                                                                                                                  /FTId=VAR_003894.
MISSING (IN ZUC).
/FTId=VAR_003895.
F -> Y (IN OMM).
                                                                                                                                                                                                                                                                             INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                         Score 1133; DB
Pred. No. 2.1e-6
                                                                                                                                                                                                                                                                                                                                                                                         HINGE.
CH2.
CH3.
                                                                                                                                                                                                                    REMOVED POST-TRANSLATIONALLY.

QV -> EB (IN ZUC).
                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. ..).
                                                                                                           /FTId=VAR
                                                                                                                                                                                                                                               INTERCHAIN
                                                                                                                                                                                                                                                              INTERCHAIN
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                                                                                                                                                                                                                                                       NTERCHAIN
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MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81007873; PubMed=6774012; Wang A.-C., Tung E., Fudenberg H.H.; Wang Arc., Tung E., Fudenberg H.G.; The primary structure of a human IgG2 heaevolutionary, and functional implications J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Linkage and sequence homology of two human immunoglobulin gamma
                                                REVISIONS TO 25; 59;
Hofmann T., Parr D.M
Submitted (MAR-1980)
                                                                                                                                                                                                                                                                                                                    "The amino acid sequences of the three heavy domains of a human IgG2 myeloma protein."; Can. J. Biochem. 57:758-767(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi N., Ueda S., Obata M., Nikaido "Structure of human immunoglobulin gamma evolution of a gene family."; Cell 29:671-679(1982).
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Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                 immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
                                                                                                                                                                                          "A note of the amino acid sequence
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(Rel. 40, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  943; PubMed=6811139;
Ueda S., Obata M.,
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                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
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MIM; 147110; -.
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_MHC.
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InterPro; IPR003597; Ig_c1.
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MIM; 147130; -.
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Mammalia; I
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
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PDB; 1ADQ; 16-SEP-98
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P01730;
  Hodge T.W., Sasso D.R., McDougal J.S.;
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                                                                                                                                                                                                                                                                                                                          MEDLINE=89028665; PubMed=3263213; Littman D.R., Maddon P.J., Axel R.; "Corrected CD4 sequence."; Cell 55:541-541(1988).
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MEDLINE=85254948; Puk
Maddon P.J., Littman
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Mammalia; Eutheria;
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man D.R., Godfre
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PubMed=1708753;
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Muzny D.M., Lu
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42, Last annotation update)
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Primates;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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                                                                               MEDLINE=92317088;
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                                                                                                   PALMITOYLATION
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                                                                                                                                                            human CD4.
                                                                                                                                                                            "Dimeric
                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
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                                                                                                                                      387:527-530(1997).
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                                                                                 PubMed=1618861;
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DR GOLOWISCHE FORCELL PROCESSION AS.

DR MIM; 186940; ...

DR MIM; 186940; ...

DR GO; GO:0012101; C:T-cell receptor activity; NAS.

DR GO; GO:0015026; F:coreceptor activity; NAS.

DR GO; GO:0015026; F:coreceptor activity; TAS.

DR GO; GO:0015029; F:internalization receptor activity; TAS.

GO; GO:0004888; F:transmembrane receptor activity; TAS.

DR GO; GO:0004896; F:transmembrane; NAS.

DR GO; GO:00045056; P:posthive regulation of interleukin-2 biosyn. ..;

DR GO; GO:0045056; P:T-cell differentiation; NAS.

DR GO; GO:0030217; P:T-cell differentiation; NAS.

DR GO; GO:00045059; P:T-cell selection; NAS.

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ..;

DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ..;

DR InterPro; IPR000973; CD4 TCA9.

DR InterPro; IPR0003596; Ig_V:

DR PRINTS; PR00602; CD4TCANTIGEN.

DR PRINTS; PR00602; CD4TCANTIGEN.

DR SMART; SM00406; IGv1 1.

DR SMART; SM00406; IGv1 1.

Tmmunoglobulin domain; Transmembrane; Glycoprotein; Palmitate; 3D-struc
    EMBL; M12807; AAA35572.1; -.
EMBL; M47924; AAB51309.1; -.
EMBL; M47924; AAA51009.1; -.
EMBL; BC025782; AAH52782.1; -.
EMBL; BC025782; AAA16069.1; -.
EMBL; BAA16069.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor interaction. May regulate T-cell activation SUBINIT: Associates with p56-lck.
SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type SIMILARITY: Contains 1 immunoglobulin-like V-type d DATABASE: NAME-PROW; NOTE-CD guide CD4 entry; WMW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".
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uiteDB; P01730; -.
HGNC:1678; CD4.
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                                                                                    IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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P16004;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
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                                                                                                                                                                                                     "A CD4 domain important for outside the virus binding Cell 60:747-754(1990).
                                                                                                                                                                                SEQUENCE OF 26-424 FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                   Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                           Camerini
                                                                                                                                                                                                                                                      MEDLINE=90182664;
                    FUNCTION: Accessory protein for MHC class-II antigen/T-ce receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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S-palmitoyl cysteine.
S-palmitoyl cysteine.
R -> W (in OKT4-negative populations).
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
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EMBL; X73323; CAA51749.1; -.
PIR; B32722; RWCZT4.
HSSP; P01730; 1WIQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:00150289; F:MFC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0006956; P:positive regulation of interleukin-2 biosyn.
GO:0045086; P:positive regulation; ISS.
GO:0030217; P:T-cell deferentiation; ISS.
GO:0045058; P:T-cell selection; ISS.
GO:007169; P:transmembrane receptor protein tyrosine kin.
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MEDLINE=85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;

"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P03987;
23-OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound form
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3.

SMART; SM00407; IGc1; 2.

PROSITE; PS00835; IG_KIKE; 3.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin

Transmembrane; Alternative splicing.
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EMBL; V01526; CAA24767.1;
PIR; A02156; G3MSM.
HSSP; P01857; 1FC1.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Mammalia; Eutheria; Rodentia;
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InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 11:6775-6785(1983).
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                                             280
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                                                                                                                                                                                                                                                                                                      Similarity
                        QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                    LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
                                                                                                                                                                                       SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCPPGNI
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Ig_MHC.
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CYTOPLASMIC (POTENTIAL).

E -> Q (IN REF. 2).

E -> Q (IN REF. 2).

P -> F (IN REF. 2).
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Pred. No. 2.8e-57;
0; Mismatches 58;
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HINGE.
CH2.
CH3.
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CF7F264B50A41B95
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RESULT 8
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21-JUL-1986 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 gamma-1 chain C region, membrane-bound for
EMBL; V00793; CAA24172.1; -.
EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
PIR; B02159; GIMSM.
                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-44 FROM N.A.

MEDLINE-82222190; PubMed=6283537;

Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T
"Nucleotide sequences of gene segments encoding mi
immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D.,
"mRNA for surface immunoglobulin gamma chi
conserved transmembrane sequence and a 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTW
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Eisenberg D., Wall R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and complete nucleotide sequence gamma 1 chain gene."; Cell 18:559-568(1979).
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Takahashi N., Mano Y.;
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MEDLINE=80045036; PubMed=115593;
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Sciurognathi;
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RESULT 9
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DT 10-OC
DE T-Cel
DE T4/Le

CD4 MACFA P79185;

STANDARD;

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15-JUL-1998 (Rel. 3 15-JUL-1998 (Rel. 3 10-OCT-2003 (Rel. 4 T-cell surface glyc T4/Leu-3).

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36, Created)
36, Last sequence update)
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annotation update)
CD4 precursor (T-cell

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MGD; MGI:96446; 1gh-4.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00407; IGc1; 2.
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SMART; SS000407; IGc1; 2.
SMO0407; PS50835; IG LIKE; 3.
PROSITE; PS000290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane; 3D-structure.
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1AE6;
1CL7;
1F11;
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                                                             GLQLDETCAEAQDGELDGLWTT
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GLQLDETCAEAQDGELDGLWTT
                                QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
                                              QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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18-MAR-98.
12-JAN-00.
06-FEB-01.
29-DEC-99.
24-JUL-02.
11-MAY-02.
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Matches 183
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GO; GO:0042101; C:T-cell receptor activity; ISS.
GO; GO:0042289; F:MCC class II protein binding; ISS.
GO; GO:0042289; F:MC class II protein binding; ISS.
GO; GO:0006955; P:Inmune response; ISS.
GO; GO:0006955; P:Dositive regulation of interleukin-2 bic
GO; GO:0001217; P:T-cell differentiation; ISS.
GO; GO:0001217; P:T-cell selection; ISS.
GO; GO:0045088; P:T-cell selection; ISS.
GO; GO:0045089; P:T-cell selection; ISS.
GO; GO:0007169; P:transmembrane receptor protein tyrosine
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR0003596; Ig_v.
Pfam; PP00047; ig; 2.
Pfam; PP00047; ig; 2.
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DOMAIN
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Tatsumi M., Yabe M., Yamada Y.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                             TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D63349; BAA09673.1; -. HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae;
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                    Immune response; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PR00692; CD41
SM00406; IGV;
                                                            \vdash
                                                                                                       Similarity
                                                     MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50835; IG_LIKE; 1.
 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                                                                                                                                                                                                                                                                                                                                                   domain; Transmembrane; Glycoprotein; T-cell; e; Repeat; Signal; Lipoprotein; Palmitate.

BY SIMILARITY.
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                                                                                                                                                   50872
                                                                                                       38.0%;
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                                                                                                                                                                                                                                                                              POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.
                                                                                                                                                N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S-palmitoyl cysteine (
S-palmitoyl cysteine (
S-palmitoyl cysteine (
                                                                                       Score 916.5;
Pred. No. 1.4e
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor protein tyrosine kin.
                                                                                                                                                                                                                                                                                                                                                                                       SURFACE GLYCOPROTEIN CD4.
                                                                                                     ; DB 1;
                                                                                                                                                   CRC64;
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                                                                                                                   Length
                                                                                                                                                                (By similarity)
(By similarity)
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RESULT 10

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OC EUART
OC HABNI
RA HASNI
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                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:MC class II protein binding; ISS.
R GO; GO:0042289; F:MC class II protein binding; ISS.
R GO; GO:0045086; P:positive regulation of interleukin-2 bic
GO; GO:00045086; P:positive regulation; ISS.
R GO; GO:00012; P:T-cell differentiation; ISS.
R GO; GO:000179; P:T-cell selection; ISS.
R GO; GO:0001799; P:T-cell selection; ISS.
R GO; GO:000973; CD4 TCAg.
R InterPro; IPR007110; Ig-Tike.
R InterPro; IPR007110; Ig-Tike.
R InterPro; IPR007110; Ig-Tike.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sec
10-CCT-2003 (Rel. 42, Last an
T-cell surface glycoprotein Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
  DOMAIN
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TRANSMEM
                                                                                                                                                         SMART; SM00406; 10v; 1.

SMART; SM00406; 10v; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin domain; Transmembrane; Glycoprotein; T-ce

Immune response; Repeat; Signal; Lipoprotein; Palmitate.

BY SIMILARITY.

BY SIMILARITY.

CIDFACE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                    PRINTS; PR00692; CD4; SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D63348; BAA09672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
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(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
ace glycoprotein CD4 precursor (T-cell surface antigen
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POTENTIAL.

CYTOPLASMIC (BOTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.
                                                                                                                                        EXTRACELLULAR
                                                                                                                                                                    SURFACE GLYCOPROTEIN
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Best Local S
Matches 175
                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequences of gene segments immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2
-i- ALTERNATIVE PRODUCTS:
Event=Alternative
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SEQUENCE
    PIR; ;
PDB; ;
PDB; ;
PDB; ;
                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-82222190; PubMed-6283537;
Yamawaki-Kataoka Y., Nakai S., Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01865;
21-JUL-1986
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GCAM_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -JUL-1986 (Rel. 01, Created)
-AUG-1991 (Rel. 19, Last sequence update)
-OCT-2003 (Rel. 42, Last annotation updat
gamma-2A chain C region, membrane-bound
s musculus (Mouse)
  ; A02154; G2MSAM.
; 1KB5; 08-APR-98.
; 1YEE; 15-OCT-97.
; MGI:96443; Igh-1.
                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                         IsoId=P01864-1; Sequence=External;
Note=Probably the major isoform;
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                            Name=Secreted;
                                                                                                                                                                                                                                                                                                                                                          Name=Membrane-bound;
IsoId=P01865-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms=2;
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                                                                              J00471; AAB59661.1;
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A. 79:2623-2627(1982)
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segments encoding
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No. 3.8e-54;
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MBL outstation -
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RESULT 12
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Matches 173
                                                                                                                                       CD4_MACMU STANDARI
P16003; Q29617;
01-AFR-1990 (Rel. 14, C
28-FEB-2003 (Rel. 41, I
10-OCT-2003 (Rel. 42, I
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SEQUENCE FROM N.A.
MEDLINE=90182664; PubMed=2107024;
Camerini D., Seed B.;
"A CD4 domain important for HIV-mediated outside the virus binding site.";
Cell 60:747-754(1990).
[2]
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                                                                            Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Cr

Mammalia; Butheria; Primates; Ca

Cercopithecinae; Macaca.
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InterPro;
InterPro;
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                                                                                                                                T-cell surface glycoprotein
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SMART; SM00407; IGc1; 2
                                                                  NCBI_TaxID=9544;
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PROSITE; PS00290; IG_MIC; 1.
Immunoglobulin domain; Immunoglobulin
Transmembrane; Alternative splicing; 3
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; IPR003006;
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42, Last annotation update)
ycoprotein CD4 precursor (T-
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14; Mismatches
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IG-LIKE 3.
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N-LINKED (GLCNAC...)
                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
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EMBL; D63347; BAA09671.1; -.
EMBL; X73326; CAA51752.1; -.
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InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the
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Mol. Biol. Evol. 15:892-900(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 107-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hashimoto O., Tatsumi M.; "Molecular cloning and expression of macaque CD4s."; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                          TRANSMEM
                                                                                                                                                                        Immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
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                                                                                                                                                                                 Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELIULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                  GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:00142289; F:MHC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0030217; P:T-cell differentiation; ISS.
GO:0045058; P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                        GO:0007169; P:transmembrane receptor protein tyrosine
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                                                                                                                                                                                                                                                                                                                                                                            AF057385; AAC25129.1; -.
                                                                                                                                                                        response; Repeat;
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PS50836; IG_LIKE; 1.
cobulin domain; Transmembrane; Glycoprotein; T-cell;
cobulin Repeat; Signal; Lipoprotein; Palmitate.
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  1WBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                             a license agreement (See http://www.isb-sib.ch/announce/
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BY SIMILARITY.
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BY SIMILARITY.
S-palmitoyl cysteine
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                             N-LINKED
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       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                    Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity of cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hashimoto O., Tatsumi
Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                             01-FBB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T.cell surface glycoprotein CD4 precursor (T-
                                                                                                                                                                                                                                                                                                                                                                                         CD4 MACNE
Q08340; P79196;
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                                                                                                                                                                                                                                                                                    Cercopithecinae;
                                                                                                                                                                                                                                                                                                                  Macaca nemestrina
                                                                                                                        -!- FUNCTION: Accessory protein
                                                                                                                                                                                      MEDLINE=93049640; PubMed=1425921;
                                                                                                                                                                                                   TISSUE=Blood
                                                                                                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                                                      NCBI_TaxID=9545;
                                                                                                                                     immunodeficiency virus.";
sur. J. Immunol. 22:2973-2981(1992).
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
 21-JUL-1986 (Rel. 01, Created)
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Immune response; Repeat; Signal; Lipoprotein; Palmitate.
SIGNAL 1 25 BY SIMILARITY.
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P01730;
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S-PARMICOY! Cysteine (1)
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C-> H (IN REF. 2).
N-> D (IN REF. 2).
N-> D (IN REF. 2).
D-> E (IN REF. 2).
D-> E (IN REF. 2).
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CYTOPLASMIC (POTENT)
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
N-LIKE C2-TYPE 3.
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  SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr.,
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83299917; PubMed=6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding
heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                   HSSP; P01857; 1FC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pratt D.M., Mole L.E.;
"Sequence studies on the constant region immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
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Bernstein K.E., Alexander C.B., Mage
"Nucleotide sequence of a rabbit IgG
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"Sequence studies of the Fd section
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                                                                                                                                                                                                                                                                          European
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                                                                                                                                                                                            A91749; GHRB
                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collable een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in fied and this statement is not removed. Usage by and for conties requires a license agreement (See http://www.isb-sib.ch/arties requires a license agreement (See http://www.isb-sib.ch/arties.
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IG-LIKE 2.
IG-LIKE 2.
IG-LIKE 3.
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T -> A (IN 1
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V -> VPV (II
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CON
                                                              SEQUENCE OF 69-133 AND 312-329.

MEDLINE=71058486; PubMed=5538616;

Turner K.J., Cebra J.J.;

"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";

Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                       MEDLINE-71058471; PubMed-5538606; Birshtein B.K., Hussain Q.Z., Cebra J.J.; Birshtein B.K., Hussain Q.Z., Cebra J.J.; Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thalf-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE 329
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-!- MISCELLANEOUS: This chain was
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
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Trischmann T.M., Cebra J.J.;
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InterPro; IPR003597;
InterPro; IPR003006;
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Q08338; O02805; (
Q1-FEB-1995 (Rel
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STANDARD; PRT; 45 12805; 077593; Q28217; 15 (Rel. 31, Created) 14 (Rel. 43, Last sequence upd 14 (Rel. 43, Last annotation u

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EMBL; AR001228; AAB60873.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF0501228; AAB60875.1; -.

R EMBL; AF0501380; AAC25124.1; -.

R HSSP; P01730; IWIQ.

R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0015028; F:coreceptor activity; ISS.

R GO; GO:00045299; F:MCC class II protein binding; ISS.

R GO; GO:0006958; P:immune response; ISS.

R GO; GO:0045086; P:positive regulation; ISS.

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0030217; D:T-cell selection; ISS.

R GO; GO:0030217; D:T-cell selection; ISS.

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . .

R InterPro; IPR000107; IgTike.

R InterPro; IPR003596; Ig_v.

P Pfam; PF00047; 13; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris E.E., Disotell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini).";

MOL. Biol. Evol. 15:892-900(1998).

-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.

-I- SUBUNIT: Associates with p56-lck (By similarity).

-I- SUBCELULAR LOCATION: Type I membrane protein.

-I- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.

-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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MEDLINE-98017879; PubMed-9379478;

Fommsgaard A. Mueller-Trutwin M.C., Diop O., Hansen J.,

Corbet S., Barre-Sinousei F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fomsgaard A., Hirsch V.M., Johnson P.R., "Cloning and sequences of primate CD4 molecules: diversity collular receptor for similar immunodeficiency virus/human immunodeficiency virus.", Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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"Molecular cloning and
Submitted (JUL-1996) to
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               CD4TCANTIGEN
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TWTCTVSQDQNTVEFKIDIM
          TWTCTVLQNQKKVEFKIDIV
                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                       ILGKQGSFLTKGSSKLRDRIDSRKSLMDQGCFSMIIKNLKIEDSETVICEVENKKEEVEL
                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSG
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BY SIMILARITY:
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S-palmitcyl cysteine (By similarit
K -> N (IN REF. 2 AND 3; AAB60873).
I -> T (IN REF. 3; AAB60873 AND 4)
G -> V (IN REF. 3; AAB60873).
F -> L (IN REF. 3; AAB60873).
K -> B (IN REF. 3; AAB60873).
N -> H (IN REF. 3; AAB60873).
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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RESULT 17
GCBM_MOUSE
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P01867;
                     MEDLINE=82222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata 'Yamawaki-Kataoka Y., Nakai S., Miyata 'Yamawaki Gene segments "Nucleotide sequences of gene segments immunoglobulin gamma chains ", Proc. Natl. Acad. Sci. U.S.A. 79:2623-:
                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                     21-JUL-1986 (Rel.
01-AUG-1991 (Rel.
15-MAR-2004 (Rel.
SEQUENCE
                                                                                  SEQUENCE
                                                                                                         NCBI_TaxID=10090;
                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                        Ig gamma-2B chain
                                                                                  OF 335-405
OF 335-378 FROM
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19, Last sequence update)
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C region, membrane-bound fo
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                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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InterPro; IPR007110; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000407; ig; 3.
SMART; SM00407; IGcl; 2
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                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC; Immunoglobulin_domain, Immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00462; AAB59659.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; 3D-structure; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82115295; PubMed=6799207;
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                                                                             78 QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF 132
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                                          PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                                                   ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF 228
 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                           PPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
                                                                                                                                LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
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                                                                                                                                                                                  36.4%; Score 877.5;
51.7%; Pred. No. 5e-1
tive 52; Mismatches
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01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J00451; -; NO
PIR; B02156; G3MSC.
HSSP; P01857; 1FC1.
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Mus musculus (Mouse)
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PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85027161; PubMed=6092053; Wels J.A., Word C.J., Rimm D., De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00407; IGc1
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InterPro; IPR003597;
InterPro; IPR003006;
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              280
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                                                                                                                                                         Similarity
                                                                                                                  SVSQLELQDSGTW-----TCTVLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCP--EL
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                                      LGGPSVF1FPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
                                                              LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                                                                                           SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS
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                                                                                                                                                                                                                                                                                         C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                         8.6e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.P., Martinez H.M.,
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                                                                                                                                                                     DB 1;
                                                                                                                                            57;
                                                                                                                                                                     Length 329;
                                                                                                                                             Indels
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                                                                                                                                            15;
                                                                                           SCPPGNI
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Best Local !
                                                                                                                                            Best Local Similarity Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAT 19
                                                                                                                                                                              GCB RAT
P20761;
01-FEB-1991
                                                                                                                                                                                                                                                                                                Pfam, PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin_domain; Immuno
                                                                                                                                                                                                                                                                                                                                            PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 gamma-28 chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rati
                                                                                                                                                                                                                                                                                                                                                                                         Gene 74:473-482(1988).
-I- SIMILARITY: Contains 3 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      Brueggemann M.;
                                                                                                                                                                                                                                                                                                                                                                                                         Evolution of the rat immunoglobulin gamma heavy-chain gene
                                   185
245
                344
                                                     284
                                                                       125
                                                                                       224
                                                                                                                           179
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                                                                                                         70
        TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                       SGTW-----TCTVLQ--NQKKVEFKIDI------VPCPAPEPKSCDKTHTC--PELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSWLQGEIFTCSVVHEALHNHHTQKNLSRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
TEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLNVERSRWD
                                                                    SVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQPREEQYNS
                                                                                                         SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
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232
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147
253
333 AA;
                                                                                                                                             Conservative
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207
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INTERCHAIN
INTERCHAIN
INTERCHAIN
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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Pred. No. 3.9e-49;
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                                                                                                                                                                               55F8B64D48D460A6
                                                                                                                                             Mismatches
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HLIM)
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Best Local &
Matches 163
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000477; Ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG MIC; 1.
Immunoglobulin domain; Immunogl
                                                                                                                                                                                                            DOMAIN
DOMAIN
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig gamma-1 chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GC1_RAT
P20759;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 74:473-482(1988).
PIR; PS0017; PS0017.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Brueggemann M.; "Evolution of the
                                                                                                                                                                                                                                                                                                           DOMAIN
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NON_TER
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 240
                 346
                                                                                     226
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                                   180
                                                                     120
                                                                                                                    183 ---TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG------PSV
                                                                                                                                                                          al Similarity
163; Conserv
                                                                                                      78
                                                                                                                                         28
                                 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                                        FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
                                                                                                      QTVTCNVAHPASSTKVDKKI-----VPRNC-----GGDCKPCICTGSEVSSV
                                                                                                                                                         LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
NEVSITCMVKGFYPPDIYVEWQMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKEKWQQG
                                                                    FIFPFKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTF
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113
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                                                                                                                                                                                                                                                                                                                                                                                                                                    rat
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112
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                                                                                                                                                                                                             35946 MW;
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                                                                                                                                                                                                                                              INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                         Score 823.5; DB 1;
Pred. No. 1.7e-48;
3; Mismatches 55;
                                                                                                                                                                                                                                                                                          CH1.
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013BAB45EF49B9DA CRC64;
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; Murinae; Rat
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NVFSCSVMHEALHNHYTQKSLSLSPG

431

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GCC_RAT

ID GCC_RAT

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AC P2076

DT 01-FE

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Best Local S
Matches 151
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DISULFID
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-2C chain C region.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCC_RAT
P20762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88166903; PubMed=3127222; Brueggemann M., Delmastro-Galfre P., Waldmann H., Calab "Sequence of a rat immunoglobulin gamma 2c heavy chain region cDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-1ike.
InterPro; IPR0075597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S00847; S00847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
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  191
                                                                                          131
                                                                                                                                                                                                                                179
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                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                  Similarity
                          LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 353
                                                                                        QHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYTIPPPREQMSKNKVSLTCM
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                                                                                                                                                                                  SSTWSSQTVTCSVAHPATKSNLIKRIEP-RRPKPRPPTDICSCDDNLGRPSVFIFPPKPK
                                                                                                                                                                                                                           SGTW-----TCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK 233
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                                                                                                                                                                                                                                                                                                                                                                     36571 MW;
                                                                                                                                                                                                                                                                           34.1%; Score 823; DB 1;
58.5%; Pred. No. 1.8e-48;
tive 45; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin
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INTERCHAIN
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CH2.
CH3.
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Cell 18:559-568(1979).
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J. Biol. Chem. 253:6068-6075(1978).
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MEDLINE=80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding
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Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., S
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., S
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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Mammalia; Eutheria; Rodentia;
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Svasti J., Milstein C.;
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Takahashi N., Mano Y.;
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MEDLINE=8118976; PubMed=6262729;

MEDLINE=8118976; PubMed=6262729;

Yamawaki-Kataoka Y., Miyata T., Honjo T.;

"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes; further evidence for intervening sequence-mediated domain transfer.";

Nucleic Acids Res. 9:1365-1381(1981).

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Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
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"Structure of the constant and 3' untranslated
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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PIR; A02152; G2MSA.
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"Petermination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Impl
for the evolution of immunoglobulin structure and function.
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; 1E4X; 12-JUL-01.
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                                                                                                                                                                                                                                                                                                                                                       Ig gamma-2A chain C region sec
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
             This
                                                                                                                                                               Dognin M.J., Lauwereys M., Strosberg A.D.; "Multiple amino acid substitutions between murine gamma chain Fc regions of Igla and Iglb allotypic forms."; Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                              MEDLINE=82037777; PubMed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P01865-1; Sequence=External; MISCELLANEOUS: The sequence differs from that of the from BALB/c mice, at 15% of the positions. SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                      Name=Secreted;
IsoId=P01864-1; Sequence=Displayed;
                                                                                                                                           SUBCELLULAR LOCATION: Secreted ALTERNATIVE PRODUCTS:
                                                                                Note=Probably the major Name=Membrane-bound;
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SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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T 10-OCT-2003 (Rel. 42, Last annotation update)
E 19 gamma-2A chain C region.
S Rattus norvegicus (Rat).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebra; Mammalia; Eutheria; Rodentia; Sciurognathi; Muri (NCBI_TaxID-10116;
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PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50230; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
                      MEDLINE=89232738; PubMed=3149946;
                                  SEQUENCE FROM N.A.
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PDB; 1HI6; 08-FEB-01.
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IG-LIKE 3.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_IKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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SIMILARITY: Contains 3 immunoglobulin-like domains.
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                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation updat
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(T-cell surface antigen T4/Leu-3)
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Cercopithecinae; Cercocebus. NCBI_TaxID=9531; [1]
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
Eur. J. Immunol. 22:2973-2981 (1992).
-i- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
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EMBL; X73328; CAA51754.1; -.

REMBL; X73327; CAA51753.1; -.

REMBL; X73327; CAB51753.1; -.

REMBL; X73327; CAA51753.1; -.

R PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin domain; Transm PRINTS; PR00692; CD4TC SMART; SM00406; IGV; 1 response; Repeat; Lipoprotein; 370 392 <1 99 177 291 CD4TCANTIGEN. 369
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316 Transmembrane; BY SIMILARITY.
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S-palmitoyl cysteine (
MISSING.
T -> I.
N -> D.
F -> L.
V -> M.
R -> K. N-LINKED (GLCNA BY SIMILARITY. BY SIMILARITY. IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3. N-LINKED POTENTIAL.
CYTOPLASMIC (POTENTIAL). EXTRACELLULAR Palmitate. Glycoprotein; (POTENTIAL). ---(By (POTENTIAL)
(POTENTIAL) T-cell; similarity)
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                                                                     EMBL; X73324; HSSP; P01730; HSSP; P01730; G0:00042101 G0; G0:0015026 G0; G0:0004228 G0; G0:00045086 G0; G0:00045086 G0; G0:00045086 G0; G0:00045086 G0; G0:00045058 G0; G0:00045058 G0; G0:00045058 G0; G0:0007169
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Q08339;
                        InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Erythrocebus.
NCBI_TaxID=9538;
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01-FEB-1995 (Rel. 31,
10-OCT-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Blood;
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Eur. J. Immunol. 22:2973-2981(1992).
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                                                                    GO:0042101; C:T-cell receptor complex; ISS.
GO:0042109; F:coreceptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0045209; F:Mc class II protein binding; ISS.
GO:004508; P:immune response; ISS.
GO:004508; P:positive regulation of interleukin-2
GO:0030217; P:T-cell differentiation; ISS.
GO:004508; P:T-cell selection; ISS.
GO:007159; P:transmembrane receptor protein tyrosi
                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content if and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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el. 42, Last annotation update)
glycoprotein CD4 (T-cell surface
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; Primates; Catarrhini; Cercopithecidae;
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                Tucker P.W., Marcu K.B., Newell N "Sequence of the cloned gene for 2b immunoglobulin heavy chain.", Science 206:1303-1306(1979).
                                                          SEQUENCE FROM N.A.
MEDLINE=80081502; PubMed=117549;
MEDLINE=80081502; PubMed=11 N.,
Marcu K.B., Newell N.,
                                                                                                                                         SEQUENCE FROM N.A. (MPC 11).48;
MEDLINE=80081501; PubMed=117548;
Tucker P.W., Marcu K.B., Slightom J.L., Blattne
"Structure of the constant and 3' untranslated
gamma 2b heavy chain messenger RNA.";
Science 206:1299-1303(1979).
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MEDLINE=80120716; PubMed=6766534;
Yamawaki-Kataoka Y., Kataoka T.,
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21-JUL-1986 (Rel. 01, Last seq
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15 gamma-2B chain C region sec
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence of cloned from newborn nouse DNA.";
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(Immune response; Repeat; Lipoprotein; Palmitate.
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Rodentia;
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Pred. No. 1.1e-45;
0; Mismatches 13
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Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00407; IGc1; 2.

SMART; SM00407; IGc1; 2.

PROSITE; PS0035; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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MEDLINE=94216359; FubMed=7512967;

Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K
Irimura T., Takahashi N., Kato K., Arata Y.;

"O-glycosylation in hinge region of mouse immunoglobulin
J. Biol. Chem. 269:12345-12350(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMĀIN
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Nature 296:761-763(1982).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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InterPro; IPR003597;
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HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: The a allele sequence is shown. SIMILARITY: Contains 3 immunoglobulin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBOIGEPO1867-1; Sequence=External; PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH MODIFIED WITH 2 SIALIC ACID RESIDUES.
PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Membrane-bound,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                        183
229 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                                                                                                                                     161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P01866-1; Sequence=Displayed;
Note=May be the major isoform;
                                                                                                                                                                                                      Similarity
                                                                                                                                 LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW---
                                    QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
                                                                    ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                                                                          LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
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Pred. No. 1.2e
iO; Mismatches
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T -> A
T -> A
T -> C
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IG-LIKE 2.
IG-LIKE 3.
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(IN ALLELE B).
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N ALLELE B).

N ALLELE B).

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N REF. 2 AND 3).

R REF. 2 AND 3).
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RESULT 29
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Q29037;
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GO; GO:004228; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0042289; P:immune response; ISS.
GO; GO:004508; P:positive regulation of interleukin-2
GO; GO:004508; P:T-cell differentiation; ISS.
GO; GO:0030217; F:T-cell differentiation; ISS.
GO; GO:004508; P:T-cell selection; ISS.
GO; GO:0007169; P:tranamembrane receptor protein tyrosi
                                                                                                                                      InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                           EMBL; D86588; BAA13131.1; -. HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                       SIGNAL
                                                                                                            PRINTS; PR00692; CD4TC SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain:
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatsumi M., Hashimoto
Submitted (AUG-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9521;
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                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I-cell surface
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                                                                                ROSITE; PS50835; IG_LIKE; 1.
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                                                                   response; Repeat;
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35, Last sequence update)
42, Last annotation update)
ycoprotein CD4 precursor (T-cell
 25
457
395
417
457
                                       Signal; Lipoprotein; Palmitate.
BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN
             EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                 T-cell;
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Cebinae; Saimiri.
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CD4_CANFA
AC P33705;
AC P37615;
AC P37625;
AC P37626;
AC MADITALID=94376;
AC MADLINE=94376;
AC MEDLINE=94376;
AC MEDLINE=
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Best Local S
Matches 143
                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Beagle; TISSUE=Thymus;
STRAINE=94378217; PubMed=8091416;
MEDLINE=94378217; PubMed=8091416;
Gorman S.D., Frewin M.R., Cobbold
Gorman S.D., Frewin M.R., Cobbold
               DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
DISULFID
DISULFID
DISULFID
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 13-463 FROM N.A.
STRAIN=Beagle; TISSUE=Thymus;
MEDLINE=93192324; PubMed=7916632;
Milde K.F., Conner G.E., Minz D.H., Alejandro R.;
"Primary structure of the canine CD4 antigen.";
Biochim. Biophys. Acta 1172:315-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
T-cell surface glycoprotein CD4 precur
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

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S-palmitcyl cysteine (By s.

S-palmitcyl CYSTEENE (BY s.
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precursor (T-cell
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No. 1.0
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ia; Canidae;
                                                                                                                                                                                                                         Waldmann
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(POTENTIAL)
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similarity)
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Matches 162
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GO; GO:0042101;
GO; GO:0015026;
GO; GO:00162289;
GO; GO:0006955;
GO; GO:0045086;
GO; GO:0045086;
GO; GO:0045088;
GO; GO:0007169;
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DISULFID
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SIGNAL
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PRINTS, PRO0692; CD4TCANTIGEM.

SMART; SM00406; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

Immunoglobulin domain; Signal; Lipoprotein; Palmitate.

TOTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L06130; AAB02295.1; -.
EMBL; X68565; -; NOT_ANNOTATED
HSSP; P01730; 1WBR.
                                            180
                                                                                         120
                                                                                                               121
                                                                                                                                      61
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                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                  SQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPK
                                                                                                               LVFGLTA--
                                                                                                                                      ILGNQGSFWTVGSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVEL
                                                                                                                                                            ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                     PKDTLMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
                                                                                          LVFNLTAKWDSGSSSGSSNIRLLQGQQLTLTI
                                            SWPELQDGGTWTCIISQSQKTVEFNINVLVLAF--
                                                                                                                                                                                                                                                                         389
463
                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P:immune response; ISS.
P:positive regulation of interleukin-2
P:T-cell differentiation; ISS.
P:T-cell selection; ISS.
P:transmembrane receptor protein tyrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:T-cell receptor complex; ISS. F:coreceptor activity; ISS. F:MHC class II protein binding;
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401
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; Ig-like.
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34.7%;
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

BY SIMILARITY.

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BY SIMILARITY OF the ine (E S-palmitcyl Cysteine (E S-palmitcyl Cysteine (E N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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LSFEDENLVGELRWQAQGAS-
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2; Mismatches
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RESULT 31

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FRANTS; PRO0692; CDATCANTIGEN.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-ce
Immune response; Repeat; Signal; Lipoprotein; Palmitate.
SIGNAL 1 25
CHAIN 26 459
T-CELT
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M92840; AAA31198.1; -.

PIR; A46254; A46254.

HSSP; P01730; IMBR.

GO; GO:0042101; C:T-cell recepto
GO; GO:0042101; C:T-cell recepto
GO; GO:0042805; F:GOreceptor act
GO; GO:0042895; P:Immune respons
GO; GO:0042896; P:T-cell differer
GO; GO:0030217; P:T-cell differer
GO; GO:0030217; P:T-cell defecti
GO; GO:0007116; P:T-cell defecti
GO; GO:0007116; P:T-cell defecti
GO; GO:0007116; P:T-cell defecti
GO; GO:0007169; P:T-cell defecti
GO; GO:00007169; P:T-cell defecti
GO; GO:0007169; P:T-cel
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01-NOV-1995 (Re
01-NOV-1995 (Re
10-OCT-2003 (Re
T-cell surface
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CD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (see or send an email to license@isb-sib.ch).
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MEDLINE=92390370; PubMed=1518821;
MEDLINE=92390370; Pub
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Mammalia; I
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GO:0042101; C:T-cell receptor complex; ISS.
GO:0042203; F:coreceptor activity; ISS.
GO:0042289; F:MHC class II protein binding; ISS.
GO:0042289; F:MHc class II protein binding; ISS.
GO:0045086; P:positive regulation of interleukin-2 |
GO:0045086; P:positive regulation; ISS.
GO:0030217; P:T-cell differentiation; ISS.
GO:0045058; P:Transmembrane receptor protein tyrosi
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 47, Last annotation update)
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Metazoa; Chordata; (
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Lagomorpha; Leporidae; Oryctolagus.
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CD4 RAT STANDARD; PRT; 457 AA. P05540; O1-NOV-1988 (Rel. 09, Created) O1-NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) T-cell surface glycoprocein CD4 precursor (T-cell T4/Leu-3) (W3/25 antigen).
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                                                                                                                                                                 LHQDWLNGKEYKCKVS-NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT-KNQVSLT
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IG-LIKE C2-TYPE
IG-LIKE C2-TYPE
IG-LIKE C2-TYPE
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S-palmitoyl cysteine
; B323311CBD40013D CR
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Pred. No. 2.7
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RAX PRAISE RAX PARA P
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                                        MEDLINE=93262437; PubMed=8493535;
Brady R.L., Dodson E.J., Dodson G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                                            <-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)</pre>
                                                                                                                                                                                                                                  immunoglobulin-related domains.";
roc. Natl. Acad. Sci. U.S.A. 84:1649-1653(1987)
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xa, Chordata, Craniata, Vertebrata, E
la: Rodentia, Sciurognathi, Muridae,
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R GO; GO:0042101; C:T cell receptor complex; ISS.
R GO; GO:0042101; C:T cell receptor activity; ISS.
R GO; GO:0042208; F:MCC class II protein binding; ISS.
R GO; GO:0042085; P:positive response; ISS.
R GO; GO:0045086; P:positive regulation of interleukin-2 biosyn
R GO; GO:0030217; P:T-cell differentiation; ISS.
R GO; GO:0030217; P:T-cell selection; ISS.
R GO; GO:0045088; P:T-cell selection; ISS.
R GO; GO:0045088; P:T-cell selection; ISS.
R GO; GO:0045088; P:T-cell selection; ISS.
R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin
InterPro; IPR007110; IGA TCAB.
R InterPro; IPR007110; Ig-Tike.
R InterPro; IPR003199; Ig.
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GO; GO:0042101; C:T-cell :
GO; GO:0015026; F:corecept
GO; GO:0042289; F:MHC clas
GO; GO:0045086; P:positive
GO; GO:0030217; P:T-cell :
GO; GO:0045088; P:T-cell :
GO; GO:0045088; P:T-cell :
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cei
Immunoglobulin domain; Signal; Lipoprotein; Palmitate;
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                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; i
PRINTS; PR00692; CD
SMART; SM00409; IG;
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                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-1ck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CD4TCANTIGEN
 domains 3
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POTENTIAL:
CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKED (GLCNAC. . . ) ()

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RESULT 33
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Best Local
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Mammalia; Eutheria; Rodentia;
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                    TISSUE=Brain;
MEDLINE=88152875; PubMed=3326818;
                                                                                                                Nature
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MEDLINE=87115821; PubMed=3027575;
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Tourvieille B., Gorman S.D., Fiel
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                           "Unusual
                                                                                                                                                                             Littman D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                325:453-455(1987)
                                                                                                                                  CD4 (L3T4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSGTWTCTVLQNQKKVEF--KIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELWVFRVTFNPGTRLLQGQSLTLILDSNPKVSDPPIECKHKSSNIVKDSKAFSTHSLRIQ
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)4 (L3T4) gene.
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Pred. No. 3.3e-26;
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thi; Muridae; Murinae; Mus
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Bittalenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny G.K., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Cheneration and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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SEQUENCE FROM N.A. (ISOFOKM 1.).
SEQUENCE FROM N.A. (ISOFOKM 1.).
STRAIN=C57BL/6J; TISSUE-Mammary gland;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=2388257; PubMed=12477932;
MEDLINE=3288257; PubMed=12477957;
MEDLINE=3288257; PubMed=12477957;
MEDLINE=3288257; PubMed=12477957;
MEDLINE=3288257; PubMed=124779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86233454; PubMed-3086886;
Classon B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
"Partial primary structure of the T4 antigens of mouse and sheel assignment of intrachain disulfide bonds.";
Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86166694; PubMed-3082751; Classon B.J., Tasgaratos J., Kirs: Brandon M., McKenzie I.F.C., Walk: "The L3T4 antigen in mouse and the immunoglobulin-like."; Immunogenetics 23:129-132(1986).
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Gibbs R.A.;
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Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
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Gorman S.D., Tourvieille B., Parn
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                                                                                     IsoId=P06332-2; Sequence=VSP_002489;
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                               receptor interaction. May regulate T-cell activat
SUBUNIT: Associates with p56-lck (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
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IsoId=P06332-2; Sequence=VSP_(
                                                                                                                                                                                                                                                                                                  IsoId=P06332-1;
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GO; GO:0042101; C:T-cell receptor complex; ISS.

GO; GO:0015026; F:coreceptor activity; ISS.

RGO; GO:0015026; F:coreceptor activity; ISS.

RGO; GO:0042289; F:MHC class II protein binding; ISS.

RGO; GO:0045086; P:positive regulation of interleukin-2 bio RGO; GO:0045086; P:positive regulation of interleukin-2 bio RGO; GO:0030217; P:T-cell differentiation; ISS.

RGO; GO:0030217; P:T-cell differentiation; ISS.

RGO; GO:0045058; P:T-cell differentiation; ISS.

RGO; GO:003217; 
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Matches 104
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EMBL; X04836; CAA28539.1; -.
EMBL; M36851; AAA39402.1; -.
EMBL; M17080; AAA37403.1; -.
EMBL; M17078; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; AC002397; AAC36010.1; -.
EMBL; BC039137; AAH39137.1; -.
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                                                                                                                                                                                                                                                             SEQUENCE
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CHAIN
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(mmune response; Repeat; Signal; Lipoprotein; Palmitate;
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                     117
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SM00406; IGV; 1
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EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                     KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
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S-palmitoyl cysteine (By s:
S-palmitoyl cysteine (By s:
Missing (in isoform 2).
/FTId=VSP 002489.
/FIDAT527CB00F33 CRC64;
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CYTOPLASMIC (POTENTIAL).

IG-LIKE CYTYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                         Score 475; DB 1;
Pred. No. 7.3e-25;
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21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 epsilon chain C region.
Mus musculus (Mouse).
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REVISIONS.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SMART; SM00407; IGc1; 2.
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RESULTING POLICY AND P
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Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL)
MEDLINE-75059123; PubMed-4803843;
Watanabe S., Barnikol H.U., Horn J., Bertr
                                                                                                REVISIONS (GAL).
MEDLINE=81066716;
                                                                                                                                                                                             "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mtype), subgroup H III. Architecture of the complete IgM-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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GO; GO:0003823; F:anti
GO; GO:0006955; P:immu
                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"Cloning and partial nucleotide sequence of human immunoglobulin mu
"Cloning and from B cells and mouse-fundan hybridomas.";

Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).

-I- MISCELLANEOUS: All 4 combinations of the S/G and V/G polymorphic
at positions 192 and 216 have been observed in human mu chains.
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SMART; SM00407; IGc.; 1G. LIKE; 4. PROSITE; PS000290; IG_MHC; 3.
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MIM; 147020; -.
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VARIANT
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Dolby T.W., Devuono J., Croce C.M
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Putnam F.W., Florent G., Paul C., Sh:
"Complete amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                    CARBOHYD
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J. Biochem.
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chain of
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            KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                             LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                              TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
ILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                              AREQUNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHS
                                                                   SRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYS
                                                                                                                    OYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOP-REPOVYTLPP
                                                                                                                                                                                                                                         SVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESG
                                                                                                                                                                                                                                                                SPSVQCR-----SPR-----GKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                           SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                          SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG
                                                                                                                                                                   LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                           PTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       454 AA;
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                                                                                                                                            -VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISES
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                                                                                                                                                                                                                                                                                                                                                                                                   15.9%;
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                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 384.5; DB 1
Pred. No. 8.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_003903.
V -> G (in dbsNP:12365).
/FTId=VAR_003904.
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435
                      431
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P01873;
21-JUL-1986 (Rel. C
01-NOV-1991 (Rel. 2
10-OCT 2003 (Rel. 4
                                                                                                                                                                                                                          Ig mu chain C region membrane-bound form.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

MCBI TaxID=10090;
                                                                     Rogers J., Wall R.;
                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                "Two mRNAs can be produced alternative RNA processing Cell 20:313-319(1980).
                                                                                                                                                                                            SEQUENCE OF 433-476 FROM N.A. MEDLINE=80222874; PubMed=6771020;
                                                                                  MEDLINE=80222873;
Rogers J., Early
                                                                                                                                                                               Early P.,
                                                                                                                                                                                                                                                                                                                                            MUCM MOUSE
                                                                             21.2]
3EQUENCE OF 410-476 FROM N.A. (MYELLO...
3EQUENCE OF 420-476 FROM N.A. (MYELLO...
3EQUENCE OF 410-476 FROM N.A. (MYELLO...)
                                                          Two mRNAs with different 3'
Event=Alternative splicing; Named Comment=During differentiation,
                       ALTERNATIVE PRODUCTS:
                                     3 of immunoglobulin
20:303-312(1980).
                                                                                                                                                                                Rogers J.,
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                         42,
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                                                                                                                                                                                Davis M.,
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Last annotation update)
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pathways.";
                                               chain.";
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isoforms=2;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V00821; CAA24; PIR; A02167; MHMSM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative eplicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P01872-1; Sequence=External; MISCELLANEOUS: The sequence of residues 1-409 is assumed to be identical with the corresponding region of the secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Secreted;
                283
                                            226
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                                                                                                                                                                                                                                                                                                                                             Similarity
              STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                        --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                            ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                        VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                    SPP-----GSSP---SVQCR----SPR-----GKNIQGG---
                                                                                                                                                                                                                TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF
                                                                                                                                                                                                                                           ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                                                                                                                                                                                                                                                                       VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed.
                                                                     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                   YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST--
                                                                                                                                                                                                                                                                                                   VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
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476
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52656 MW;
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25.2%;
87;
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N-LINKED (GLCN)
N-LINKED (GLCN)
                                                                                                                                                                                                                                                                                                                              Score 373.5; DB
Pred. No. 5.2e-1
7; Mismatches 1
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BY SIMILARITY
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INTERCHAIN
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LINKED (GLCNAC...).
LINKED (GLCNAC...).
8D476575A5204071 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .).
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DOMAIN 205
DOMAIN 314
CONFLICT 168
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P01855;
21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                               MEDLINE=821/73/0, MEDLINE=821/73/0, Bennich H.;
Hellman L., Pettersson U., Bennich H.;
"Characterization and molecular cloning of the mRNA
(epsilon) chain of rat immunoglobulin E.";
Proc. Natl Acad. Sci. U.S.A. 79:1264-1268 (1982).
Proc. Natl Acad. Sci. U.S.A. 79:1264-1268 (1982).
-!- SIMILARITY: Contains 4 immunoglobulin-like doma:
                                                                                             Pfam; PF00047; ig; 4.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 3
                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                              EMBL; J00744; AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.; "A cloned cDNA probe for rat immunoglobulin epsilon heavy construction, identification, and DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  CONFLICT
                                                                                                                                             InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                    HSSP; P01854;
                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=82174576; PubMed=6803238;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 205-306 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA 1:335-343(1982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 168-342 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 10:6041-6049(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellman L., Pettersson U., Engstroem A., Karlsson "Structure and evolution of the heavy chain from 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=83064537; PubMed=6292865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LOU/C/WSL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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 103
205
205
314
168
308
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(Rel. 42, Last annotation update)
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                                                                                                                                                                                                        AAA41379.1; ALT_INIT.
                                                                                    domain;
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Sciurognathi; Muridae; Murinae; Rattus.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
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P04221;
20-MAR-1987
01-NOV-1991
10-OCT-2003
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Bernstein K.E., Alexander C.B., Reddy E.P., M
"Complete sequence of a cloned cDNA encoding of VHa2 allotype: comparisons with VHa1 and m
J. Immunol. 132:490-495(1884).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987 (Rel. 04, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 mu chain C region membrane-bound form.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EutMammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this stratement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                    PIR; A02165; MHRBM.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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Comment-During differentiation, B lymphocytes so
expression of isoform Membrane-bound to isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Membrane-bound;
IsoId=P04221-1; Se
                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P03988-1; Sequence=External;
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Pred. No. 7.2e
52; Mismatches
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RESULT 39

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                                               DIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                        EYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
                                                                                                                                                                                                                                                                                          NDRADSRRSLWDQGNFFLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL
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LPHMVTERTVDKS----TEGEVGAEEEGFENLWTT
                  LHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                      DVFVQWQQRGQPLSSDKYVTSAPAPEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEA
                                                                            QFTCTVTHADLPFPLKHTISKSREVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPA
                                                                                                                    VTDLTTYG-SLNISW-----ASHNGKALDTHMNITESHPNATFSAMGEASVCAEDWESGE
                                                                                                                                        VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                           FFDKNVSMSSECSTTPSP------
                                                                                                                                                                           QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                  SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
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Pred. No. 9.7e-18;
9; Mismatches 153
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RESULT 40
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Matches 119
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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HSSP; P01857; 1FC1
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"Amino acid sequence of the Fc region of a interspecies homology for the IgM class.";
Science 200:1159-1161(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCumber L.J., Capra J.D.;
"The complete amino-acid sequence
Mol. Immunol. 16:565-570(1979).
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MEDLINE=80077682; PubMed=117299;
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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119; Conserv
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                                                              LYNVSLVLSDTAGZ
                                                                                                                                   KTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG---
                                                                                                                                                           ISKAKG-QPREPQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNY
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                                                                                                              VTSAPMPEPQAPGLYFAHSILTVSEEEWNAGETYTCVVAHESLPNRVTERSVDKSTGKPT
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                                                                                     LQLDETCAE
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   STANDARD;
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Pred. No. 9.7e
80; Mismatches
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DOMAIN
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20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig mu heavy chain disease protein (BOT).
Il general sequence (Human).
Eukaryota, Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The primary structure of mu-chain-disease protein amino-acid sequence of the N-terminal 42 positions Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 3
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HSSP; P01857; 1FC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005624; C:membrane fraction; NAS. GO; GO:0003823; F:antigen binding; TAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Barnikol-Watanabe S., Mihaesco E.,
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                                                                                              RFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCLVTGFSPA
LPNRVTERTVDKSTG 372
                                                                    DIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                  EYKCKYSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
                                                                                                                                              KLTCLVTDLTTYD-SVTISWTRQDGEAVKTHTNISESHPNATFSAVGEASICEDDWDSGE
                                                                                                                                                                      EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
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                                                                                                                                                                                                                                                                                                                    EVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR-------
                      LHNHYTQKSLSLSPG
                                                DVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEA
                                                                                                                                                                                                                       -QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS-----VFLFPPKPKDTLMISRTP
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391 AA;
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156
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261
391
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(NO V REGION
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RESULT 41

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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_MHC.
Pfam; PP00047; Ig; 4.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
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P01872;
21-JUL-1986
21-JUL-1986
10-OCT-2003
                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                       EMBL; V00827; -; N
PIR; A02166; MHMS.
HSSP; P01857; 1FC1
                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Auffray C., Rougeon F.;
"Nucleotide sequence of a cloned cDNA corresponding to secreted chain of mouse immunoglobulin.";
Gene 12:77-86(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-82051295; pubMed=6795090; Goldberg G.I., Vanin E.F., Zrolka A.M., "Sequence of the gene for the constant I Balb/c mouse immunoglobulin."; Gene 15:33-42(1981).

SEQUENCE FROM N.A. (MYELOMA TEPC183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81076590; PubMed-6255422;
Kawakami T., Takahashi N., Honjo T.;
"Complete nucleotide sequence of mouse immunoglobulin mu comparison with other immunoglobulin heavy chain genes.";
Nucleic Acids Res. 8:3933-3945(1980).
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISION (MOPC 104E).
MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-79223904; PubMed=111247;
Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W.,
"Anino acid sequence of a mouse immunoglobulin mu chair
Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (MYELOMA PROTEIN MOPC 104E)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete amino acid sequence of a mouse mu heavy chain constant region domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (MYELOMA TEPC183)
MEDLINE=81165562; PubMed=6260591;
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-JUL-1986 (Rel. 01, Last sequence up
-OCT-2003 (Rel. 42, Last annotation
mu chain C region secreted form.
musculus (Mouse)
                                                                                                                                                                                                                                                                                                                  Name=Secreted;
IsoId=P01872-1; Sequence=Displayed;
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Event-Alternative splicing; Named isoforms=2;
Event-Alternative splicing; Named isoforms=2;
Comment-During differentiation, B lymphocytes switch from
                                                                                                                                                                                                                                                                                                         Name=Membrane-bound
                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                         IsoId=P01873-1; Sequence=External;
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Sciurognathi;
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EMBL; L00022; AAB59424.1; ALT_INIT.
PIR; A22771; EHHU.
PDB; 11GE; 15-JUL-92.
PDB; 1FP5; 30-JAN-02.
PDB; 1684; 16-MAY-01.
PDB; 100V; 18-SEP-02.
Genew; HGNC:5522; IGHE.
MIM; 147180; ---
GO; GO:0003823; F:antigen binding; NA
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MEDLINE=84207910; PubMed=6327276;
Weda S., Nakai S., Nishida Y., Hisajima H.,
"Long terminal repeat-like elements flank a
"Long terminal repeat-like introns.";
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"The sequence of
region gene, and
EMBO J. 1:655-660
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(In) Bach
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MEDLINE=83001945; PubMed=6288268;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
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                                                                                                                                                                                                                                                                                               This
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"A model of the Fc of immunoglobulin
Mol. Immunol. 23:1063-1075(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A. MEDLINE=83065234; PubMed=6815656; MEDLINE=83065234; PubMed=6815656; MEDLINE=83065234; PubMed=6815656; Medline M., Molgaard H.V., Houghton M., Derbyshire Bell L.O., Gould H.J.; Gould H.J.;
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MEDLINE=83168897; PubMed=6300763;

MEDLINE=83168897; PubMed=6300763;

Seno M., Kurokawa T., Ono Y., Onda H., Sasada
Seno M., Kurokawa T., Ono Y., Onda H., Sasada
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;

"Molecular cloning and nucleotide sequencing
epsilon chain cDMA.";
epsilon chain cDMA.";
Nucleic Acids Res. 11:719-726(1983).
                                                                                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING.
MEDLINE=87089848; PubMed=3796618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marcel Dekker, New York (1978).
[6]
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Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom
(In) Bach M.K. (eds.),
Immediate hypersensitivity: modern concepts and dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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., Rabbitts T.H.;
e of a human immunoglobulin epsilon and evidence for three non-allelic
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                                                                                                                                                                                                                                                                                                                                                of VHa2 allotype: comparisons with VHa1 and membrane mu . Immunol. 132:490-495(1984).
-i- SUBCELLULAR LOCATION: Secreted (Probable).
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (A2 ALLOTYPE).
MEDLINE=84088930; PubMed=6418803;
Bernstein K.E., Alexander C.B., Reddy E.P., M
"Complete sequence of a cloned cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g mu chain C region secreted form.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalis, Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                             Thie
                                                                                    between
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on the European Bioinformatics Institute. There are no restrictions on way by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                              Name=Secreted,
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Comment=During differentiation, B lymphocytes switch
expression of isoform Membrane-bound to isoform Secre
                                                                                                                                                                                       IsoId=P03988-1; Sequence=Displayed;
Name=Membrane-bound;
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LHNHYTQKSLSLSPG
                   DVFVQWQQRGQPLSSDKYVTSAPAPEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEA
                                                                                                              VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                             VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR------
                                                                                                                                                                                                                                                                                      NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL
                                                                                                                                                                                                                                                                                                                            AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
                                      DIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
                                                          QFTCTVTHADLPFPLKHTISKSREVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPA
                                                                             EYKCKVSNKALPAPIEKTISKAKGQPRE-PQVYTLPPSRDELT-KNQVSLTCLVKGFYPS
                                                                                                  VTDLTTYG-SLNISW-----ASHNGKALDTHMNITESHPNATFSAMGEASVCAEDWESGE
                                                                                                                                           FFDKNVSMSSECSTTPSP
                                                                                                                                                              QNOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                  SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                                                                                                                                    -----GKNIQGG------KTLSVSQLELQDSGTW-----TCTV----L
                                                                                                                                                                                                                                                                                                          ALTDGNLVAMG------
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                 -SSRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
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23.8%;
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BY SIMILARITY.
INTERCHAIN (WITH HEAVY OF SY SIMILARITY.
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Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                          CLARDFLPSSVTFSWSFKNNSEI-------
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                                                                                                                                          -GIQVFPIAPSFADT-FLSKSARLICL
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P20768;
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                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 4. SMART; SM00407; IGc1; 3
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
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01-FEB-1991 (Rel. 17,
16-OCT-2001 (Rel. 40,
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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LPHMVTERTVDKSTG
--OLEGAT
                LPAATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
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                                                                                            Conservative
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                                                                                           N-LINKED
N-LINKED
                                   Score 354.5; DB 1;
Pred. No. 9.4e-17;
1; Mismatches 163;
                                                                                                                      N-LINKED
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INTERCHAIN (WITH HEAVY
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ID MUC MESAU
AC P06337;
DT 01-JAN-1988
DT 01-FEB-1996
DT 15-JUL-1999
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                                                                      EMBL; X02804; CAA26574.1; -.
HSSP; P01854; 1ICE:
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003596; Ig_MHC.
Pfam; PP00047; ig; 4.
SMART; SM00407; IGC1; 2.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=85297761; PubMed=2994005;

McGulire K.L., Duncan W.R., Tucker P.W.;

"Phylogenetic conservation of immunoglobulin
"Phylogenetic conservation of conservation of immunoglobulin
comparison of hamster and mouse Cmu genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last sequence u
15-UUL-1999 (Rel. 38, Last annotation
Ig mu chain C region.
Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                             NON TER
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Rodentia;
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RESULT 46
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Best Local S
Matches 115
 SEQUENCE FROM N.A.
MEDLINE=88328985; Publ
Kokubu F., Hinds K., 1
"Complete structure as
                                                                                                                                   -HVC2 HETFR
P23085;
01-NOV-1991
01-NOV-1991
10-OCT-2003
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain C region (Clone 12022) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthye
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontiae; Heterodontus.
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K., Litman R., Shamblott M.J., Litman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constant region genes in a phylogenetically primitive vertebrate."; EMBO J. 7:1979-1988(1988).
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PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 3.
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    -!- SIMILARITY: Contains 4 immunoglobulin-like domains.

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                                                               LTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSDG-SFFLYSKLTVDKSRWQQGN
                                                                                               NISTQAWLSGAEFYCVVSHQDLPTPLRASIHKEEVKDLREPFVSVLLPPAEDVSAQRFLS
                                                                                                            TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVS
                                                                                                                                                                                                                SGTWTCTVLQNQKKVEFKI--DIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTL
                                                                                                                                                                                                                                            TVLCSIIDFHPESITVSWLKDGQPMDSGFVTSPTCEVNG----NFSATSRLTVPAGEWFS
                                                                                                                                                                                                                                                                   -----LQGQSLTLT-----LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQD
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 SYSCVVGHEAI PLKI INRTVNKSSG
                      VFSCSVMHEALHNHYTQKSLSLSPG
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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IG-LIKE 3
IG-LIKE 4
N-LINKED
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Pred. No. 6.4e-14;
7; Mismatches 155
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"Nucleotide sequence of the constant r
chain immunoglobulin mRNA.";
Nucleic Acids Res. 11-5--
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Ig mu chain C region.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
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InterPro; IPR003597; Ig cl.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 1.
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PIR; A02170; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 3.
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01-NOV-1991
15-JUL-1999
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01-NOV-1991 (Rel. 20, Last sequence update)
01-VOV-1991 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain C region, membrane-bound form (Clone 3050).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes
Flasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                            constant region genes in a phylogenetically primitive vertebrate."; EMBO J. 7:1979-1988(1988).
                                                                                   EMBL; X07781; CAA306:
PIR; S01854; HVRKCO.
                                                                                                                                                                                                                                                                         MEDLINE=88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman
"Complete structure and organization of immunoglobulin
                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVLCSPSDSVYTVGCAAFDFQPSSIAFTWFDSNNSSVSGM--DVIPKVISGPPYRAVSR-
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InterPro; IPR007110; 1
InterPro; IPR003597; 1
InterPro; IPR003006; 1
Pfam; PF00047; 1g; 4

Ig-like. Ig_c1. Ig_MHC.

SM00407;

HSSP; P01842;

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CZ HUMAN

CZ PO1877;

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SEQUENCE
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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
   SEQUENCE FROM N.A. MEDLINE=84130179;
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90; IG_MHC; 3.
domain; Immunoglobulin
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       PubMed=6421489;
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Primates;
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Pred. No. 8.9e-13;
                                                                                                                                                 Craniata; Vo
Catarrhini;
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                                                                                                                                                 Vertebrata; Euteleostomi; i; Hominidae; Homo.
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 2
                                                                                                                                                                                                                                                 GO; GO:0005624; C:membrane fraction; NA
GO; GO:0003823; P:antigen binding; TAS:
GO; GO:0006955; P:immune response; NAS:
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
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                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                EMBL; J00221; AAB59396.1;
PIR; B22360; B22360.
HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=79180140; PubMed=286295; Tsuzukida Y., Wang C.-C., Putnam F "Structure of the A2m(1) allotype
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"Mechanisms of divergence and
alpha-1 and alpha-2 constant r
Cell 36:681-688(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete amino acid sequence of the alpha 2 he IgA2 immunoglobulin of the A2m (2) allotype."; Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=78137069; PubMed=416441; Torano A., Putnam F.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomeric or polymeric.
MISCELLANEOUS: The sequence of the A2m(1) allotype is
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Ig alpha is the major immunoglobulin class secretions. It may serve both to defend against local and to prevent access of foreign antigens to the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunologic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structure and function of hem. J. 271:285-296(1990).
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allotype of human IgA --
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nce of the human
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                        Heterodontus francisci (Horn shark).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;

Heterodontidae; Heterodontus.

NCBI_TaxID=7792;
                                                                       MEDLINE=88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain
constant region genes in a phylogenetically primitive vertebrate.";
EMBO J. 7:1979-1988(1988).
                                                                                                                                                                                                                                                       P23087;
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P -> S (IN A2M(2))

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P -> R (IN A2M(2))

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F -> Y (IN A2M(2))
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Pred. No. 7.1e-13;
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/FTId=VAR_
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I (IN A2M(2)
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E (IN A2M(2)
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R (IN A2M(2)
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 . Usage by and for commercial http://www.isb-sib.ch/announce/
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                                          a collaboration - MBL outstation -
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Query Match
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SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 4

PROSITE; PS00290; IG_MHC; 3.
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                                                                                                                    DKSVNPGNYKNTEVMAENDNSSYPIYSLLSIAAEEWASGASYSCVVGHEAIPLKIINRTV
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                                                                                          SLSPG
                                                                                                                                             GQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
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Ig_c1.
Ig_MHC.
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N-LINKED
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5; Mismatches
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Pred. No. 1e-12;
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RESULT 52
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Matches 78
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NON TER 1
DOMAIN 71
DOMAIN 174
SEQUENCE 299
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SMART; SM00407; IGc1; 2.

PROSITE; PS00290; IG_MHC; 2.

Immunoglobulin domain; Immunoglobulin C
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Oryctolagus
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"Genes encoding alpha-heavy chains of rabbit IgA: characterization of the coding IgA-g subclass alpha-chains.";
Nucleic Acids Res. 12:1657-1670(1984).
-I- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02174; AHRB.
HSSP; P01857; 1FC1.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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SIMILARITY: Contains 2 immunoglobulin-like domains.
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                                                                                                                                              275
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                                                                                                                                                                                                  LSLSPG
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cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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           STANDARD;
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276 IG
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SEQUENCE
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01.NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain C region (Clone 6125) (Fragment).
Heterodontus francisci (Horn shark).
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DOMAIN
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SMART; SM00407; IG
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EMBO J. 7:1979-1988(1988)
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MEDLINE-88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
Complete structure and organization of immunoglobulin heavy chain
"Complete structure and organization of immunoglobulin heavy chain
"Complete structure and organization of immunoglobulin heavy chain
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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PS50835; IG_LIKE;
PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                GSSKIYCEVRRGESLWIKEIPDCKGDIVHPTVILTQTSSBEITSSRFATVVCSIIDFHPE
VDISTQAWLSEAVFYCVVSHQDLPTPLRDSIHKEAWKDLREPSVSVLLPPAEEISAERFL
                                      LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLPPSRDELTKNQ-V
                                                                                                                                                                                                                                                                                                                         VQLLVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                 GPSKLNDRADSRRSLW-----DQGNFPLIIKNLKIEDSD----
                                                                                                                                   LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVVSV
                                                                                                                                                                                   WFTNTVYTCQVSHQAATQSRNI - - - - TGSPDSSECNH - -
                                                                                                                                                                                                                             LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                           ----AITVNWLKDGHPMESGFVT
                                                                                         L-LEATVILICY
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370
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26.2%;
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IG-LIKE 2.
IG-LIKE 3.
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N-LINKED (G
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N-LINKED (C
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Pred. No. 2.7
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  (See http://www.isb-sib.ch/announce/
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                                                                                       -TQEQKPLKSEIAVQPGEDPDSVIST
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
If heavy chain C region (Clone 6121) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88328985; PubMed=3138109;
Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain constant region genes in a phylogenetically primitive vertebrate.";
EMBO J. 7:1979-1988(1988).
                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
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01-NOV-1991
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                      23
 4
                                                          Similarity
                      TQGNKV----VLGKKG----DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
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 TTGLKTYPSVLNKKGTYTQSSQLTITESE---
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26.4%;
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Pred. No. 6.9e
69; Mismatches
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IG-LIKE 2.
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                                              161;
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01-FEB-1991
10-OCT-2003
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_GORGO
              Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                           ALC1
                                                                                Ig alpha-1 chain C region.
NCBI_TaxID=9595
                                                                 IGHA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGQSLTLT-----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCT 185
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                                                                                           (Rel. 17, Created)
(Rel. 17, Last sequence up
(Rel. 42, Last annotation
                                                                                                                                                           STANDARD;
                                                                                                             update)
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PBS0835; IG_LIKE; 3.
PROSITE; PBS0835; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                    Kawamura S., Omoto K., Ueda S.;
"Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.";
Nucleic Acids Res. 17:6732-6732(1989).

-!- FUNCTION: Ig alpha is the major immunoglobulin class in body
secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                     entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymph node;
MEDLINE=89386006; PubMed=2506527;
                                                                                                         HSSP; P01810;
                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        immunologic system.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                       X15045; CAA33147.1; ALT_INIT.
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                                                          ; Ig-like.
; Ig_cl.
; Ig_MHC.
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MEDLINE=88130179; PubMed=6421489;
Flanagan J.G., Lefranc M.-F., Rabbitts T.H.;
"Mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences.";
[2]
                                                                                                   P01876;
21.-UL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
To alpha-1 chain C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80114124; PubMed=393607;
Yang C.-Y., Kratzin H., Gotz H., Hilschmann N.,
"Rule of antibody structure. Primary structure
IgA-immunoglobulin (myeloma protein Tro). VII.
characterization of the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 360:1919-1940
                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3. SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                       MIM;
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PDB; 1IGA; 15-JUN-99
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putnam F.W., Liu Y.-S.V., Low T.L.K., "Primary structure of a human limininglobulin Ighl protease, digestion, Fab and Fc fragments, a amino acid sequence of the alpha 1 heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA MEDLINE=79151016;
                                                                                                                                                                                          Polymorphism;
                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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PS00290; IG_MHC; 1.
obulin_domain; Immun
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            SEQUENCE FROM N.A.
MEDLINE-90384824; PubMed=2119496;
Wilson M.R., Marcuz A., van Ginkel
Middleton D., Warr G.W.;
                                                                                                       Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
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TPS -> PST (IN REF. 2 E -> B (IN REF. 3).
P -> S (IN REF. 3).
R -> H (IN REF. 3).
H -> R (IN REF. 3).
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Pred. No. 1e
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Pfam; SM00407; IGc1; 1.

SMART; SM00407; IGc1; 1.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 2.

Immunoglobulin domain; Immunog?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catfish, Ictalurus punctatus: an unusual mRNA splice pattern produce the membrane form of the molecule."; Nucleic Acids Res. 18:5227-5233(1990).

--- MISCELLANEOUS: During differentiation, B lymphocytes switch from expression of membrane-bound IgM to secretion of IgM. The muchains of membrane and secreted IgM differ in their C-terminal
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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InterPro; IPR003597;
InterPro; IPR003006;
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P01857; 1FC1.
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ITGPST-----EDILIKRAGQLEC----RAEGDTGFKSIKWLIGNREISSLSNL---
                         LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK-FNWYVDGVEVHNAKTKPRE
                                                      NFTAISVLELSAS-EWTSSTSPVKCEFQQKNHNVFKEASYAPGDTKQPQ-----
                                                                                 KTLSVSQLELQDSGTWT-----CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                             TPTQTEIDNGTATFVCLATP-----FSPKSHTFKWTLEKTDISNKVKENIVSQNKG
                                                                                                                                         ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRG--
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Pred. No. 2.2e
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POTENTIAL.
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EQYNSTYRVVSVLT-VLHQDWLNGKEYKCKVSNKALPAPIEK-TISKAKGQPREPQVYTL

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RESULT 57
ALC_MOUSE
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P01878;
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MEDLINE=81054880; PubMed=6776528;
Robinson E.A., Appella E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-213 (MOPC 47A). 
MEDLINE=80049769; PubMed=115869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Auffray C., Nageotte R., Sikorav J.-L., Heidmann O., Rougeon R. "Mouse immunoglobulin A: nucleotide sequence of the structural for the alpha heavy chain derived from cloned cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ig alpha chain C region.
                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                               EMBL; D11468; BAA02026.1; ALT_INIT
PIR; A91479; AHMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robinson E.A., Appella E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Amino acid sequence of a mouse myeloma immunoglobin heavy chain (MOPC 47 A) with a 100-residue deletion.";
J. Biol. Chem. 254:11418-11430(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81261947; PubMed=6790349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).";
Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outse European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in iffied and this statement is not removed. Usage by and for comittee requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                             FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general immunologic system.

MISCELLANEOUS: The final C-region domain is deleted from Ref. 2 chain. It was isolated from a myeloma protein that contains 1 light and 1 heavy chain per molecule, linked by a disulfide bond. In contrast, normal mouse IgA molecules contain 2 light and 2 heavy chains and lack a light-heavy chain disulfide bond.

MISCELLANEOUS: M511 chain was isolated from a myeloma protein that his contain 1 chain was isolated from a myeloma protein that
                                                                                                                                                                                                                               binds phosphorylcholine.

MISCELLANEOUS: M511 sequence was compared with that of mouse MOPC 47A, and a genetic mechanism for the deletion of the CH3 domain of the mutant chain is proposed.

SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the alpha heavy chain derived e 13:365-374(1981).
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               P01810;
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Q9WTN4;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)

phosphatase non-receptor type

substrate 1

precursor

STANDARD;

088555;

RT; 513 AA. O88556; P97796;

Q8R559;

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RESULT 58
SHS1_MOUSE
ID SHS1_MOUSE ST
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SMART; SM00407; IGc; 3. --
PROSITE; PS50835; IG LIKE; 3. --
PROSITE; PS00290; IG_MHC; 2.
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                           HEALHNHYTOKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                         SITCTLNGLRNPEGAV-FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWN
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                                                                                                          HEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                PSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVM
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26.7%;
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IG-LIKE 3.
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IG-LIKE 3.
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PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114; ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365, AND N-GLYCOSYLATION.
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motifs) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Brain, and Cerebellum; MEDLLNE=98012243; PubMed=9348339; Comu S., Weng W., Olinsky S., Ishwad P., Mi ; Lagenaur C.F., Narayanan V.;
 TISSUE=Placenta;
             SEQUENCE
                                                  "High-throughput sequence identification within alcohol-related QTLs.";
                                                                              Ehringer M.A., The
Beeson M., Gordon
                                                                                                        STRAIN=ILS, and ISS;
MEDLINE=21363810; PubMed=11471062;
                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-29; ARG-67; PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114; ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365.
                                                                                                                                                                                            Sano S.-I., Ohnishi H., Kubota M.; "Gene structure of mouse BIT/SHPS-1."; Biochem. J. 344:667-675(1999).
                                                                                                                                                                                                                                    STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain, and Liver; MEDLINE=20053880; PubMed=10585853;
                                                                                                                                                                                                                                                                                                                                    "High expression of inhibitory receptor with protein tyrosine phosphatase SHP-1 J. Biol. Chem. 273:22719-22728(1998).
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98380500; PubMed=9712903; Veillette A., Thibaudeau E., Latour S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphatase-binding protein family.",
J. Neurosci. 17:8702-8710(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SEQUEN
(ISOFORM 2), VARIANTS ALA-29; ARG-91; THR-96
N-GLYCOSYLATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohnishi H., Kubota M., Sano S.-I.; "BIT (Bit) maps to mouse chromosome Genomics 40:504-506(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/c; TISSUE=Brain; MEDLINE=97230468; PubMed=9073522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujioka Y., Kasuga M.; "Mouse and human SHPS-1: molecular cloning of cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) regulatory protein alpha-1) (Sirp-alpha-1) (mSIRP-alphalantigen) (Brain Ig-like molecule with tyrosine-based act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lagenaur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maur C.F., Narayanan V.;
murine P84 neural adhesion molecule
                                          Genome
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             FROM
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SER-128; PRO-194 AND AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion of genes."
                                        12:657-663 (2001)
             N.A.
                                                                             Thompson J., Conroy on L., Bennett B.,
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             (ISOFORM 1),
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Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231:61-67(1997).
              AND
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              VARIANT PRO-194
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                                                               n T.E., San of gene
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                                                                               Yang F., Canniff J.,
., Sikela J.M.;
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1) (MyD-1
                                                                    variants
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as docking protein and induces translocation of PTPNS,
PTPN11 and other binding partners from the cytosol to the
plasma membrane. Supports adhesion of cerebellar neurons, neurite
outgrowth and gilal cell attachment. May play a key role in
intracellular signaling during synaptogenesis and in synaptic
function. Involved in the negative regulation of receptor tyrosine
kinase-coupled cellular responses induced by cell adhesion, growth
factors or insulin. Mediates negative regulation of phagocytosis,
mast cell activation and dendritic cell activation. CD47 binding
prevents maturation of immature dendritic cells and inhibits
cytokine production by macure dendritic cells and inhibits
cytokine production by macure dendritic cells (By similarity).

-i- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
macrophages, where it primarily binds PTPN6. Binds GRB2 vitro.
Binds FGR. Binds JAKZ irrespective of its phosphorylation status
and forms a stable complex. Binds SCAP1 and/or SCAP2. The
resulting complex recruits FYB. Binds FYBS (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gresham H.D., Dale B.M., Potter J.W., Lowell C.A., Lagenaur C.F., Willman C. "Negative regulation of phagocytosis kinase family member, Fgr.",
J. Exp. Med. 191:515-528 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang H., Chen Z., Ullrich A.;
"Epidermal growth factor-induced association of SHP2 with alphal.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBT darabase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-GLYCOSYLATION, PHOSPHORYLATION HORMONE, AND INTERACTIONS WITH JAMEDLINE=98175985; PubMed=9507023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Growth hormone regulation of SIRP and association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stofega M.R., Wang H., Ullrich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-GLYCOSYLATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chuang W., Lagenaur C.F.; "Central nervous system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90152134;
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                                        Name=3; Synonyms=b, Small;
IsOdd=P97797-3; Sequence=VSP_007031;
TISSUE SpEGIFICITY: Highly expressed in cerebral cortex, brain, spinal cord, cerebellum and spleen, and at much lower levels in kidney, thymus, heart, lung and liver. Within the cerebellum, highly expressed throughout the molecular layer and in synaptic glomeruli in the granule cell layer. Detected in neurons of the hippocampus and dentate gyrus, and in olfactory bulb. Not detecte in Purkinje cells. Highly expressed in the plexiform layers, optifiber layer and the outer segments of the photoreceptor layer in fiber layer and the outer segments of the photoreceptor layer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem.
                                                                                                                                                                                                                                                                                Name=1; Synonyms=a;
IsoId=P97797-1; S
the retina. Highly expressed in macrophages. at very low levels in all tissues tested. DEVELOPMENTAL STAGE: Highly expressed in the day 7 to 17.
                                                                                                                                                                                                                                               Name=2; Synonyms=a', Large; IsoId=P97797-2; Sequence=
                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Immunoglobulin-like cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 273:7112-7117(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274:559-562(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10662797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2303162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.F., Narayanan V.;
ed protein is a ligand
                                                                                                                                                                                                                                                 Sequence=VSP_007032;
                                                                                                                                                                                                                                                                                    Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND TISSUE
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GO: 0045309; I
GO: 0005515; I
GO: 0007015; I
GO: 0006928; I
GO: 0007160; I
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SIMILARITY: Contains 2 immunoglobulin-like C1-type domain
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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D85785; BAA20376.1; -.
; U89694; AAB92591.1; -.
; AF072543; AAC24886.1; -.
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AF332079;
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Y10349; CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
PAPIEKTISKAKGQPREPQVYTLPPS----RDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                            SPRNITLKWFKDGQELHHLETTVNPSGKNVSYNISSTVRVV----LNSMDVHSKVICEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----WYRG-----HF------VGQSRLLIYSFTGE---HF-----
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                                                                                                                                                                                          KGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTC----KSHGF
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F:protein binding; IPI.
P:actin filament organization; IMP.
P:cell motility; IMP.
P:cell-matrix adhesion; IMP.
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AAK56107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:cytoskeletal regulator activity;
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Pred. No. 3.7e-06;
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Eur. J. Inmunol. 28:1-11(1998).

FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PTPN6, prevail and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function. Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin. Mediates negative regulation of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells (By similarity).

-i- SUBUNIT: Binds PTPN1 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro. Binds JAK2 irrespective of its phosphorylation status and forms a artshia commilex.
                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (MyD-1 antigen).
PTPNS1 OR SHPS1 OR SIRP OR MYD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHS1_BOVIN
046631; 046632;
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                                                                                                                                                                                                                                                                                                                                          stable complex. Binds SCAP1 and/or SCAP2. The resulting conrecruits FYB. Binds FGR and PTK2B (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Highly expressed in spleen macrophages Detected in skin dendritic cells.
PTM: Phosphorylated on tyrosine residues (By similarity).
                                                                                                                                                                                                                                                              PTM: Phosphorylated on tyrosine residues (By similarity). SIMILARITY: Contains 2 immunoglobulin-like C1-type domain: SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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EMBL; Y11046; CAA71943.1; -.
InterPro; IPR007111; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003006; Ig_MHC.
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PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50290; IG_MIC; FALSE NEG.
Repeat; Signal; Transmembrane; Immun
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                                                                                                                                                                                                            PHOSPHORYLATION ON TYROSINE RESIDUES.
STRAIN=Sprague-Dawley; TISSUE-Brain;
MEDLINE=97415431; PubMed=9271230;
Sano S.-I., Ohnishi H., Omori A., Hasegawa J., Ku
"BIT, an immune antigen receptor-like molecule in
FEBS Lett. 411:327-334(1997).
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P97710; 008951; 070426; Q9QWI5;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (Brain Ig-like molecule with tyrosine-based activation motifs) (Bit) (Macrophage fusion
   Saginario
Ullu E., V
                                  STRAIN=Fischer 344; TISSUE=Macrophage; MEDLINE=98449911; PubMed=9774638; Saginario C., Sterling H., Beckers C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9709866; Pubreu-03220hi T., Iwamatsu A., Yamao 1., Fujioka Y., Matozaki T., Noguchi T., Iwamatsu A., Yamao 1., Fujioka Y., Matozaki T., Rasuga M.; Takada T., Kasuga M.; Takahashi N., Tsuda M., Takada T., Kasuga M.; Takahashi N., Tsuda M., Takada T., Kasuga M.; Takahashi N., Tsuda M., Takada T., Kasuga M.; Takahashi N., Tsuda M.; Takada T., Kasuga M.; Takamatsu A., Yamao 1., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158; 174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 Al 446-453, N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, INTERACTIONS WITH PTPN6 AND PTPN11.
TISSUE=Fectal fibroblast; TISSUE=Fectal fibroblast; PubMeda8943344; TISSUE=F000867; PubMeda8943344;
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Eukaryota; Metazoa; Chor
                                                                                                                                                                                     SEQUENCE FROM N.A.
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adhesion.";
Vignery
                                                                                                                                                      446-467
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AND 496-506,
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                                                                                                                                                      OF 99-107; 128-149; N-GLYCOSYLATION, A
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2; Mismatches 139;
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                                  <u>.</u>
                                          Kobayashi
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                                                                                                                                                  9; 192-217;
AND TISSUE
                                                                                                                                                                                                                                                                                                 Kubota M.;
in the brain.";
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                                      Solimena M
                                                                                                                                                      405-417;
SPECIFICITY.
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as docking protein and induces translocation of PTN6;
PTN11 and other binding partners from the cytosol to the
plasma membrane. Supports adhesion of cerebellar neurons, neurite
outgrowth and gilal cell attachment. May play a key role in
intracellular signaling during synaptogenesis and in synaptic
function. Involved in the negative regulation of receptor tyrosine
kinase-coupled cellular responses induced by cell adhesion, growth
factors or insulin. Mediates negative regulation of phagocytosis,
mast cell activation and dendritic cell activation. CD47 binding
prevents maturation of immarture dendritic cells and inhibits
cytokine production by mature dendritic cells May play a role in
the release of nitric oxide by macrophages (By similarity).

SUBNUT: Binds PTN11 when tyrosine-phosphorylated, except in
macrophages, where it primarily binds PTN6. Binds GRB2 in vitro.

Binds FGR. Binds JAK2 irrespective of its phosphorylation status
and forms a stable complex. Binds SCAP1 and/or SCAP2. The
resulting complex recruits FYB. Binds PTX2B (By similarity).

-!- SUBCELIULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in brain, spleen, lung, liver
and kidney. Detected at lower levels in heart. Highly expressed in
dendritic cells.
                                                                                                                                                                                                                                                                                                                             This SWI
EMBL;
EMBL;
EMBL;
HSSP;
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                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    the
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-1- FUNCTION: Immunoglobulin-like cell surface receptor for CD47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takada T., Matozaki T., Takeda H., Fukunaga K., Nogue
Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F.,
"Roles of the complex formation of SHPS-1 with SHP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=WAG/Rij; TISSUE=Alveolar macrophage;
MEDLINE=98375871; PubMed=9712053;
Adams S., van der Laan L.J.W., Vernon-Wilson E.,
Renardel de Lavalette C., Doepp E.A., Dijkstra C.D.,
van den Berg T.K.;
"Signal-regulatory protein is selectively expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98204923; PubMed=9535915;
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                                                                                                                                                                                                                                                                                                                                                                              PTPN11.
SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                               ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
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; D85183; BAA12
; D38468; BAA20
; U62328; AAC68
; AF055065; AAC
; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EW
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adhesion or epi
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                                                    ; BAA12734.1; -. BAA20368.1; -. AAC68478.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osine residues in growth factors. I
                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Ochi F., Kar
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Dephosphorylated by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
 374
374
395
32
150
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274
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 373
3944
209
138
248
2248
332
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436
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                                                                                                                                                      477
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PHOSPHORYLATION AND PTPN11 BINDING; WHEN ASSOCIATED WITH F-436, F-460 AND F-477.

P -> L (IN REF. 4).

F -> I (IN REF. 4).

F -> I (IN REF. 3).

S -> C (IN REF. 3).

KR -> MP (IN REF. 3; AA SEQUENCE).

G -> A (IN REF. 3).

D -> N (IN REF. 3); AA SEQUENCE).

O -> Q (IN REF. 3; AA SEQUENCE).

G -> P (IN REF. 3; AA SEQUENCE).

G -> P (IN REF. 3; AA SEQUENCE).

NARE -> EGON (IN REF. 3; AA SEQUENCE).
                                                                                                                F-460, F-477 AND F-501.

Y->F: ABOLISHES TYROSINE PHOSPHORYLATION AND PTPN11 BINDING; WHEN ASSOCIATED WITH F-436, F-477 AND F-501.

Y->F: STRONGLY REDUCES INSULIN-INDUCED TYROSINE PHOSPHORYLATION AND PTPN11 BINDING. ABOLISHES TYROSINE PHOSPHORYLATION AND PTPN11 BINDING; WHEN ASSOCIATED WITH F-436, F-460 AND F-501.
Y->F: STRONGLY REDUCES INSULIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
SH2-BINDING
SH3-BINDING
SH2-BINDING
SH2-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE V-TYPE.
IG-LIKE C1-TYPE:
                                                                                                                                                                                                N-LINKED
N-LINKED
Y->F: ABC
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N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                    TYROSINE PHOSPHORYLATION AND BINDING. ABOLISHES TYROSINE
                                                                                                                                                                                         AND
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                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      SH2-BINDING (POT PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE PHOSPHAT
TYPE SUBSTRATE 1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; SH3-binding;
                                                                                                                                                                                   PTPN11 BINDING; WHEN ASSOCIATED 50, F-477 AND F-501.
                                                                                                                                                                                                 ABOLISHES TYROSINE
                                                                                                                                                                                                       GLCNAC
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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ASSOCIATED WITH
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PRESENTATION OF THE PRESEN
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CONFLICT
SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Ig lambda-1 chain C region.
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LAC1_MOUSE
                    MEDLINE=71107854;
                                        SEQUENCE (MYELOMA
                                                                                  "Somatic variants of muri
Nature 298:380-382(1982).
                                                                                                                            Baltimore D.
                                                                                                                                                Bothwell A
                                                                                                                                                                                                                                     Nature 290:65-67(1981).
                                                                                                                                                                                                                                                                             Gefter M.L.,
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83014953; PubMed=6812053; Seleting E., Miller J., Witson R., & Seleting E., Miller J., Witson R., & Tolking E., Miller J., Witson R., & Proc. Natl. Acad. Sci. U.S.A. 79:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01843;
                                                                                                                                                                  MEDLINE=82220143;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Bothwell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                           "Dual expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (Mouse)
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.L., Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKPEHFTDNRDGTYNYTSLFLVNSSAHREDVVFTCQVEHDSQPAITENHTVRAFAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYTQKSLSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ATKRNNM----DESICISNVTPEDAGTYYC-VKFQKGIVE------PDTEIKSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQADKSVSVAAGDSATLNCTVSSLTPVGPIKWFKGEGQNRSPIYSFIGGEHFPRITNVSD
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                                                                                                                                                                                                                                                                               Paskind M., Schwartz timore D.;
                                                                                                                                                Paskind
                                                                                                                                                                                                                                                      of lambda genes
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PubMed=6283385;
                                        PROTEIN MOPC 104E)
                    PubMed=5276767;
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22.8%;
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MISSING (IN REF. 3; AA SEQUENCE
; 5BE1FE0A4DD429F4 CRC64;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                     bulin lambda genes.";
79:4681-4685(1982).
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                                                                                                                                              Imanishi-Kari T.,
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                                                                                                                                                                                                                                                      MOPC-315 plasmacytoma.";
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01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular cell adhesion protein 1 precursor (V
VCAM1 OR VCAM-1.
                                                                                                                                                                                                  VCA1 RA
P29534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                 Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:599-594(1971).
-!- MISCELLANBOUS: The MOPC 315 cell line produces 2 light chains,
normal lambda-2 chain and 1 abnormal lambda-1 chain that is
missing a large part of the V region. The C region sequence (si
here) appears completely normal.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
MEDLINE=92181437; PubMed=1371918;
Hession C., Moy P., Tizard R., Chisholn
Burkly L., Miyake K., Kincade P., Lobb
"Cloning of murine and rat vascular cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                             SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A93922; L1MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00582; AAA51636.1; -.
EMBL; J00587; AAB59672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMĀIN
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                                                                                                                                                                                                                 RAT
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                                                                                                                                                                                                                                                                              SNNKYMASSYLTLTARAWERHSSYSCOVTHE---GHTVEKSLS
                                                                                                                                                                                                                                                                                                                                                    QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                    SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                            QPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQ 60
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35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ET -> TE (IN REF. 4)
Q -> E (IN REF. 4).
MISSING (IN REF. 4).
HS -> SH (IN REF. 4)
                                                                                                                                                                                                                                                                                                                                                                             Score 177.5; DB 1;
Pred. No. 1.2e-05;
8; Mismatches 43;
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. . .
                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE.
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             -> SS (IN REF. 4).
-> Q (IN REF. 4).
A89F2B09BCFCA018 C
                       Chisholm P.,
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                                                                                                 Murinae; Rattus.
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                        Wysk
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Query Match
Best Local S
Matches 101
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SEQUENCE
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DISULFID
DISULFID
CARBOHYD
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-i- FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1 INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL TRANSDUCTION. THE VCAM1/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES AND IN LEUKOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007310; Ig-like.
InterPro; IPR00538; Ig-c2.
InterPro; IPR003989; VCAM-1.
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M84488; AAA42332.1; -.
                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed on inflamed vascular (
well as on macrophage-like and dendritic cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 7 immunoglobulin-like C2-type domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMIGRATION TO SITES OF INFLAMMATION.
335
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CAAVGCDSPSFSWRTQTDSPLNGEVRDEGATSTLTLSPVGVEDEHSYLCTVTCQRRKLEK
                                                                                                                                                          EGAAVTMTCASEGLPAPEIFWSKK----
                                     LESPPGSSPSVQCRSPRGKNIQG-----GKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                          TLTLIAMRMEDSGIYVCEGVNLVGRDKTEVELIVQEKPFTVDISPGSQVAAQVGDSVVLT
                                                                                                               PLIIKNLKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQSLTLT
                                                                                                                                                                                             KGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                   81246 MW;
                                                                                                                                                                                                                                                         21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Cell adhesion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 7.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                     Score 176.5; DB 1
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VASCULAR CELL
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POT SC608E5A1A1B100C CRC64;
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                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                       169;
                                                                                                                                                        -LINGVLQLL-
                                                                                                                                                                                                                                    Indels 131;
                                                                                                                                                                                                                                                                        Length 739;
                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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s in both nor
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RESULT 63
SRB2_HUMA1
REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                             RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Eird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Cliston A., G., Frankland J.A., Fraser A., French L., Garner P., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Hawlor S., RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., RA Marsh V.L., Mattin S.L., McConnachie L.J., McLay K., McMurray A.A., RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., RA Miltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., RA Miltehead S.L., Whittaker P., Willey D.L., Williams S.A., Beck S., RA Rocers J., Patel R., Bebard T., Durbin R.M., Bentley D.R., Beck S., RA Rocers J., Patel R., Bebard T., Durbin R.M., Bentley D.R., Beck S.,
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QSPIWB; Q8WWA5; QSNOKB;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=21638749;
              Rogers J.;
"The DNA sequence and comparative analysis of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ichigotani Y., Matsuda S., Machida K. Yamaki K., Hayakawa T., Hamaguchi M.; "Molecular cloning of a novel human gemember of the SIRP/SHPS-1 protein fam J. Hum. Genet. 45:378-382(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21036165; PubMed=11185750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIQVEVYSFPED-----PEIEISGP-----LVHGRPVTVNCTVPNVYPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EA---GISKKSVELIIQGSSKDIQLTVFPSKSVKEGDTVIISCTCGSVPEIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an gene (SIRP-B2) which encodes a new
family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K., Oshima K., Iwamoto
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RC TISSUE-Lung:

RX MEDLINE-22388257; PubMed=12477932;

RX MEDLINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Maxin G.M., Hong L.,

RA Lithchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Wczykar P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Whiting M., Maclan A., Young A.C., Garcia A.M., Gaby L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA RAHas S., Ketteman J.W., Green E.J., Lu X.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Generation and initial analysis of more than 15,000 full-length

**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

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**Martin M.A.;** Schein J.E., Jones S.J.M., Marra M.A.;**

**Martin M.A.;** Sc
    InterPro; IPR007110; Ig-like.
InterPro; IPR003997; Ig-cl.
InterPro; IPR003997; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; Pr00047; Ig; 3.
SWART; SW00407; IGC1; 2.
SWART; SW00406; IGV; 1.
                                                                   Alternative
SIGNAL
  CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB042624; BAA95692.1; EMBL; AL138804; CAC00474.1; EMBL; BC020629; AAH20629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
Repeat; Signal; Transmembrane; Immur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
-I- FUNCTION: Probable immunoglobulin-like cell su
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     ; 605466; ...
GO:0007267; P:cell-cell signaling; TAS.
GO:0007242; P:intracellular signaling cascade; TAS.
GO:0008285; P:negative regulation of cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note-No experimental confirmation available; TISSUE SPECIFICITY: Detected in liver, and at brain, heart, lung, pancreas, kidney, placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9P1W8-3; Sequence=VSP_007028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:15757; SIRPB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9P1W8-2; Sequence=VSP_007027;
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361 383
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                        SIGNAL-REGULATORY PROTEIN BETA-2 EXTRACELLULAR (POTENTIAL).
                                                                          POTENTIAL.
                                                                                                                       Immunoglobulin
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P20767;
P20767;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
I glambda-2 chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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SEQUENCE FROM N.A.
MEDLINE=87305594; PubMed=3114047;
Steen M.L., Hellman L., Pettersson U.;
"The immunoglobulin lambda locus in rat
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CARBOHYD
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CARBOHYD
                                                   NCBI_TaxID=10116;
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100; Conservative
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                                                                                                                                                                                                         DDVVLTCQVKHDG------QLAVSKRLALEVT 348
                                                                                                                                                                                                                                                                                                                                                                                                             LODSGTWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSV-FLFPPKP
                                                                                                                                                                                                                                 QGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDET
                                                                                                                                                                                                                                                       AGNOVNVTCQVRKFYPQSLQLTWLENGNVCQRETASTLTENKDGTYNWTSWFLVNISDQR
                                                                                                                                                                                                                                                                            TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                                                                                                                  IRSTARVVLDPWDVRSQVICEVAHVTLQGDPLRGTANLSEAIRVPPTLEV-TQQPMR---
                                                                                                                                                                                                                                                                                                                       VVSVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                                                                                                                                                                            SAPVVLGPAARTTPEHTVSFTCESHGFSPRDITLKWFKNGNELSDFQTNVDPTGQSVAYS
                                                                                                                                                                                                                                                                                                                                                                 KDTLMIS----RTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                         PADVGTYYCVKFRKGSPENVEFK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP---LIIKNLKIEDSDTYICEVEDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF--LLLTLLGLTEVAGESELQMIQPEKLLLVTVGKTATLHCTVT---
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/FTIG=VSP 007028.
A -> V (IN REF. 2).
L -> S (IN REF. 2).
W; F7F20C9F86E0E64B CF
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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Pred. No. 9.2e-05;
0; Mismatches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (i
/FTId=VSP_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform SP_007027.
                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  -GHFPRVTTVSDLTKRNNMDFSIRISSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164;
                                                                                                                                                                                                                                  437
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) (POTENTIAL).
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Best Local
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InterPro; IPRO0357; Ig_cl.
InterPro; IPRO03006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_IKE; 1.
PROSITE; PS50835; IG_MHC; 1.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=Colon, and Skin;

MEDLINE=92235084; PubMed=1569102;

Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;

Murdoch A.D., Dodge G.R., Cohen I., Tuan Bulfate proteoglycan from "Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSP62/perlecan). A chimeric molecule with multidomains homologous to the low density lipoprotein receptor, laminidomains homologous to the low density lipoprotein receptor, laminidomains homologous to the low density lipoprotein factor.";
                                                                                                                                                                                                                                                                                                                                                                                             HUMAN STANDARD; PRT; 4391 AA.

POBM HUMAN STANDARD; PRT; 4391 AA.

P98160; Q16287; Q9H3V5;

01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan
protein precursor (HSPG) (Perlecan) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene
                                                                                                                                                                Kallunki P., Tryggvason K.;
Human basement membrane heparan sulfate proteoglycan core protein:
467-KD protein containing multiple domains resembling elements of the containing multiple domains resembling elements of the containing moderal lipowell in the containing moderal substitution modecules, and epidermal growth factor.";
10. Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92112994; PubMed=1730768;
Kallunki P., Tryggvason K.;
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22521; AAA41420.1; ALT_INIT.
HSSP; P01842; 2MCG.
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                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNKYIASSFLRLTAEOWRSRNSFTCOVTHE---GNTVEKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AA;
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27
103
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85
103
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                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11318 MW;
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Pred. No. 2.8e
L7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH HEAVY CHAIN).
; F087906DE43F7276 CRC64;
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.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
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L outstation -
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Kallunki P., Eddy K.L., Z.-.
Kallunki P., Eddy K.L., Z.-.
Tryggvason K.;
Tryggvason K.;
"Cloning of human heparan sulfate proteoglycan core protein,
"Cloning of human heparan sulfate proteoglycan core protein,"
"Cloning of human heparan sulfate protein,"
"Cloning of h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang H., Li X.-J., Martin D.B., Aebersold R.;
"Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
Nat. Biotechnol. 21:660-666(2003).

-I- FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.
-I- SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Heparan sulfate proteoglycan of human colon: partial cloning, cellular expression, and mapping of the gene short arm of human chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20553141, PubMed=11101850;
MICOLE S., Davoine C.-S., Topaloglu H., Cattolico L., Bar
Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hentati F., Fontaine B.;
"Perlecan, the major proteoglycan of basement membranes, i patients with Schwartz-Jampel syndrome (chondrodystrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94052171; PubMed=8234307;
Cohen I.R., Graessel S., Murdoch A.D.,
"Structural characterization of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Yi H.F., Iozzo R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Colon;
MEDLINE=91365376; PubMed=1679749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 22-439
MEDLINE=20553141;
                                                        This SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITE ASN-2121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 890-1396 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 10:673-680(1991).
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                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Extracellular.

TISSUE SPECIFICITY: Found in the basement membranes.

PYM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.

DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel Syndrome (SUS1) [MIM:255800]; a rare autosomal recessive disorder characterized by permanent myotonia (prolonged failure of muscle relaxation) and skeletal dysplasia, resulting in reduced stature, kyphoscoliosia, bowing of the disphyses and irregular epiphyses. SIMILARITY: Contains 4 LDL-receptor class A domains.

SIMILARITY: Contains 11 laminin EGF-like domains.
                                                                                                      SIMILARITY: Contains 3 laminin IV domains.
SIMILARITY: Contains 22 immunoglobulin-like C2-type
SIMILARITY: Contains 3 laminin G-like domains.
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 1 SEA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acad. Sci. U.S.A. 90:10404-10408(1993)
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R.L., Byers M.G.,
try is copyright. It is produced through Institute of Bioinformatics and the EW commatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM
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complete
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human
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between the the European

Swiss Institute Bioinformatics

restrictions

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Pfam; PF00008; EGF; 4.

Pfam; PF00007; 19; 22.

Pfam; PF00007; 1aminin_B; 3.

Pfam; PF00053; laminin_G; 3.

Pfam; PF00054; laminin_G; 3.

Pfam; PF00057; ldl_recept_a; 4.

Pfam; PF00057; ldl_recept_a; 4.

Pfam; PF00057; ldl_recept_a; 4.

Pfam; PF00057; ldl_receptor.

PRINTS; PR00261; LDLRECEPTOR.

PRODOm; PD003031; Laminin_B; 3.

SWART; SW00180; EGF_Lam; 12.

SWART; SW00180; IGC; 7.

SWART; SW00281; LamB; 3.

SWART; SW00281; LamB; 3.

SWART; SW00281; LamB; 3.

SWART; SW00282; LamG; 3.

SWART; SW00202; EGF_1; 9.

PROSITE; PS01186; EGF_2; 6.

PROSITE; PS01186; EGF_2; 4.

PROSITE; PS50026; EGF_2; 4.

PROSITE; PS50026; EGF_2; 4.

PROSITE; PS50026; EGF_3; 4.

PROSITE; PS50026; EGF
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InterPro; IPR006209; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF_
InterPro; IPR006210; IIGF_
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig_c.
InterPro; IPR003599; Ig_c.
InterPro; IPR003595; Ig_v.
InterPro; IPR003595; Ig_v.
InterPro; IPR00034; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000181; SEA_domain.
Pfam; PF000082; Laminin_B; 3.
Pfam; PF00052; Laminin_B; 3.
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EMBL; M85289; AAA52700.1; -.
EMBL; M445795; CAC18534.1; -.
EMBL; M64283; AAA52699.1; -.
EMBL; M64283; AAA52699.1; -.
EMBL; S76436; AAB21121.2; -.
EMBL; L22078; -, NOT ANNOTATED_CDS.
PIR; A38096; A38096.
HSSP, P00740; IEDM.
Siena-2DPAGE; P98160; -.
Genew; HGNC:5273; HSPG2.
MIM; 142461; -.
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LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LO-LIKE C2-TYPE 1.

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 2.
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AC 20273; O95699; O95701; O95702; O95703; Q01665
AC Q9UQA7; Q9UQA8; Q9UQA9; Q9UQA9; Q9Y2A6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE B-cell receptor CD22 precursor (Leu-14) (B-lyr)
DE molecule) (BL-CAM) (Siglec-2).
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(N EGF-LIKE 4 (INCOMPLETE).

(N EGF-LIKE 5 (N-TERMINAL).

(N EGF-LIKE 5 (C-TERMINAL).

(N EGF-LIKE 5 (C-TERMINAL).

(N EGF-LIKE 6.

(N EGF-LIKE 9 (N-TERMINAL).

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phospholipase
J. Exp. Med. 1
                                                                            Law C.L., Sidorenko S.P., Fischer E.H., Clark E.A., "CD22 associates with prot
                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH LYN; SYK AND PIK3R1/PIK3R2.

MEDLINE=96257803; PubMede8647200;

Tuscano J.M., Engel P., Tedder T.F., Agarwal A., Kehrl J.H.;

"Involvement of p72syk kinase, p53/56lyn kinase and phosphatidyl
inositol-3 kinase in signal transduction via the human B lymphoc
antigen CD22.";
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MEDLINE-9321636; PubMed-8463235;
MEDLINE-93216636; PubMed-8463235;
Powell L.D. Sgrot D. Sjoberg E.R., Stamenkovic I., Varki A.;
"Natural ligands of the B cell adhesion molecule CD22 beta carry
"Natural ligands of the B cell adhesion molecule CD22 beta carry
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"The B-cell antigen CD22 mediates monocyte and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson G.L., Fox C.H., Fauci A.S., Ke "cDNA cloning of the B cell membrane
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                                                                                                                                                                                       MEDLINE=96195207; PubMed=8627166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas M.L., Fearon D.T.;
"A role in B cell activation for CD22 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doody G.M., Justement L.B., Thomas M.L., Fearon D.T.;
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       associates with protein tyrosine phosphatase holipase C-gamma(1) upon B cell activation."; p. Med. 183:547-560(1996).
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269:242-244(1995)
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Chem. 268:7019-7027(1993).
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Annu. Rev. Immunol. 15:481-5(
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MEDLINE=97288746; PubMed=9143697;
Tedder T.F., Tuscano J., Sato S., Kehrl J.H.;
"CD22, a B lymphocyte-specific adhesion molecule that regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues.

PIM: Phosphorylated on tyrosine residues by LYN (By sim SIMILARITY: Belongs to the immunoglobulin superfamily. (sialic acid binding Ig-like lectin) family.

(SIMILARITY: Contains 6 immunoglobulin-like C2-type domai SIMILARITY: Contains 1 immunoglobulin-like V-type domai SIMILARITY: Contains 1 immunoglobulin-like V-type domai SIMILARITY: Contains 1 immunoglobulin-like V-type domai
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SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                            L; X59350; CAA42006.1; -.
L; U62631; AAB06449.1; -.
L; U62631; AAB06449.1; -.
L; X52785; CAA36988.1; ALT FRAME.
L; AB012996; BAA36565.1; -.
L; AB012999; BAA36566.1; -.
L; AB012999; BAA36567.1; -.
L; AB013000; BAA36569.1; -.
L; AB013000; BAA36572.1; -.
L; AB013000; BAA36572.1; -.
L; AB013000; BAA36573.1; -.
L; AB013001; BAA36573.1; -.
L; AB013004; BAA36573.1; -.
L; AB013006; BAA36575.1; -.
L; AB013006; BAA36575.1; -.
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DOMAIN: Contains 4 copies of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.
                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface. Upon ligand induced tyrosine phosphorylation in the immune response seems to be involved in regulation of B cell antigen receptor signaling. Plays en in positive regulation through interaction with Src family tyrosine kinases and may also act as an inhibitory receptor by recruiting cytoplasmic phosphatases via their SH2 domains that block signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the localization of B-cells in lymphoid tissues. Binds sialyla glycoproteins; one of which is CD45. Preferentially binds to alpha2,6-linked sialic acid. The sialic acid recognition site be masked by cis interactions with sialic acids on the same ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATABASE: NAME=PROW; NOTE=CD guide CD22 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd22.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAUTION: Ref. 4 sequence differs from that shown frameshift in position 806.
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                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P20273-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                             pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and for contact this statement is not removed. Usage by and for correquires a license agreement (See http://www.isb-sib.ch/ar
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PROSITE; PS50835; IG_LIKE; 6.

Cell adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein;

Cemmunoglobulin domain; Repeat; Phosphorylation; Alternative splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                              KCKVSNK--ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
                                                                    TLSCNYNSSNPSVTRYEW----KPHGAWEEPS-----
                                                                                                    CVVVDVSHEDPEV-KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                             IDIVPCPAPEPKSCDKTHTCPELLG---
                                                                                                                                                                                                               LCMSLANP---LPTNYTWYHNGKEMOGRTEEKVHIPKILPWHAGTYSC-VAEN
                                                                                                                                                                                                                                    LTLTLESPPGSSPSVQCRSPRGKNIQG--GKTLSVSQLELQDSGTWTCTVLQNQKKVEFK
                                                                                                                                                                                                                                                                                      FTLNLREVTKDQSGKYCCQVSNDVGPGRSEEVFLQVQYAPEPSTVQILHSPAVEGSQVEF
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IPR003598; Ig_c2.
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IG-LIKE C2-TYPE I
ITIM MOTIF 1.
ITIM MOTIF 3.
ITIM MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 167; DB 1; I
Pred. No. 0.00085;
D; Mismatches 154;
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 847;
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RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagglley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Ra Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Clarder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corrby N.R.,
RA Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Collson A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Collson A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Harloy B.J., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Mice C.D., Smith M.L., Soderlund C., Schra H.K., Shownkeen R., Sims S.,
RA Rice C.M., Ross M.T., Scott C.E., Schra H.K., Shownkeen R., Sims S.,
RA Michead S.L., Mittaker P., Walley D.L., Williams D.W., Thorpe A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Leck S. L., Williams J., Walliams S.A.,
Milming L., Warder P., Willey D.L., Williams S.A.,
Milming L., Warder P., Walley D.L., Walliams L., Walliams S.A.,
Milming L., Walliams S.A.,
Milming L., Warder P., Walley D.L., Walley D.L.,
Market P., Walley D.L., Walley D.L.,
M. Be
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28-FEB-2003 (Rel
10-OCT-2003 (Rel
10-OCT-2003 (Rel
MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Signal-regulatory protein beta-1 precursor (SIRP-beta-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A family of proteins that inhibit signalling receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97215901; PubMed=9062191; Kharitonenkov A., Chen Z., Sures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                         TISSUE=Skin;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363
                                                                                                                                                                                                                                 NA sequence and comparative 414:865-871(2001).
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2; Q9H1U5; Q9Y4V0;
Dell 41, Created)
                                                                                                                                                                                            N.A. (ISOFORM
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Primates;
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                                                                                                                                                                                                                                                                                                  Hubbard
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                                                                                                                                                                                                                                                         analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marxa M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                  EMBL; AL049634; CAB46661.2; -.

EMBL; AL138804; CAC17540.1; -.

EMBL; BC025286; AAH25286.1; -.

Genew; HGNC:15928; SIRPB1.
                                                                                                                                                                                                                                                                                                                                         EMBL; Y10376; CAA71404.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dietrich J., Cella M., Selffert M., Buehring H.-J., Colonna M.; "Signal-regulatory protein beta 1 is a DAP12-associated activating receptor expressed in myeloid cells."; J. Immunol 164:9-12(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomasello E., Cant C.,
Ullrich A., Vivier E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20072721; PubMed=10604985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Association of signal-regulatory proteins beta with Eur. J. Immunol. 30:2147-2156(2000).
                                                                                                                                                               MIM, 603889; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu.

InterPro; IPR007110; Ig-like.

InterPro; IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11169422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH TYROBP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH TYROBP AND SYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the negative regulation of receptor tyrosine kinase-coupled signaling processes. Participates also in the recruitment of tyrosine kinase SYK.

SUBUNIT: Interacts with TYROBP. This interaction results in recruitment of SYK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=000241-2; Sequence=VSP_007026;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in monocytes and dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Immunoglobulin-like cell surface receptor involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=000241-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buehring H.-J.,
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                    POTENTIAL.
SIGNAL-REGULATORY PROTEIN BETA-1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                          Immunoglobulin
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Best Local S
Matches 76
                                                                                   "The Caenorhabditis elegans gene unc-89, required assembly, encodes a giant modular protein compose transduction domains.";

J. Cell bio.
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SEQUENCE FROM N.A. STRAIN=Bristol N2; Du Z., Le T.T., Wi
                                                                                                                                                                             SEQUENCE FROM N.A., FUNCTION, AND STRAIN-Bristol N2;
MEDLINE-96180278; PubMed=8603916;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFSPRDITLKWFKNGNELSDFQTNVDPAGDSVSYSIHSTARVVLTRGDVHSQVI-----
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N-LINKED (GLCNAC. ..) (POTENTI
N-LINKED (GLCNAC. ..) (POTENTI
N-BERT (IN isoform 2).

/FIId=VSP 007026.
R -> H (IN REF. 2; CAC17540).
D -> N (IN REF. 1).
D -> A (IN REF. 2; CAB46661).
P -> A (IN REF. 2).
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Pred. No. 0.00045;
9; Mismatches 139;
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IG-LIKE V-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
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                                                                                                                     : muscle
                                                                                                                                                                                                                                                                                                                                                                     protein 89).
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| signal
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pfam; pF0004
pfam; pF0016
pfam; pF0016
pfam; pF0062
pfam; pF0062
sMART; SM0031
SMART; SM0032
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pROSITE; pS50
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InterPro; IPR003961; FN_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-Like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
InterPro; IPR000219; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; ...
PDB; 1FHO; 20---
PDB; CO9D1.1; (
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7fam; PF00047; fg; 47.

*fam; PF00047; fg; 47.

*fam; PF00169; PH; 1.

*fam; PF00621; RCSD; 5.

*am; PF00621; RhoGEF; 1.

**Am; PF00018; SH3; 1.

**Am; RM00408; IGC2; 23.

**Am; SM003026; RhoGEF; 1.

**T; SM003026; SH3; 1.

**TE; PS000326; SH3; 1.

**TE; PS50010; DH 2; 1.

**TE; PS50010; DH 2; 1.

**TE; PS500002; SH3; 1.
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EMBL; AF00313
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1; AAB54132.2;
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This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                   SEQUENCE OF 1-18 (MYELOMA PROTEIN CBPC-49).
Breyer R.M., Sauer R.T., Eisen H.N.;
"The variable region of mouse lambda-3 chains.";
ICN UCLA Symp. Mol. Cell. Biol. 20:105-110(1981)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=83014953; PubMed=6812053;
Selsing E., Miller J., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig lambda-3 chain C region.
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                                                                                                                             MEDLINE-81223782; PubMed-6165998; Azuma T., Steiner L.A., Eisen H.N
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                          LAC3
                                                                                                   "Identification of a third immunoglobulins.";
                                                                                                                                                                                                                                                                                        Evolution of mouse immunoglobulin lambda
                                                                       SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                         (MYELOMA
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                                                                                                               , Eisen H.N.;
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                                                                       immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 70
PGBM_MOUSE
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Matches 35
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Q05793;
Q1-NOV-1995
                               Vamada Y., Hassell J.R.;
Yamada Y., Hassell J.R.;
"Identification of cDNA clones encoding different domains of the basement membrane heparan sulfate proteoglycan.";
J. Biol. Chem. 263:16379-16387(1988).
-I- FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
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Pfam; PF00047; 1Gc1; 1.

SMART; SM00407; IGc1; 1.

PROSITE; PS50835; IG_MHC; 1.

PROSITE; PS00290; IG_MHC; 1.
            +
                                                                                                                                                                                                            sulfate proteoglycan,
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01-NOV-1995 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                  MEDLINE=89034110;
                                                                                                                                                 SEQUENCE OF 940-1601 AND 1870-2600 FROM
                                                                                                                                                                         J. Biol.
                                                                                                                                                                                     molecule.
                                                                                                                                                                                                                                     Noonan D.M., Fulle A., Valente P.,
Yamada Y., Hassell J.R.;
                                                                                                                                                                                                                                                             MEDLINE=92078153; PubMed=1744087;
                                                                                                                                                                                                                                                                          TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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properties. It serves as an attachment substrate SUBUNIT: Purified perlecan has a strong tendency dimers or stellate structures. It interacts with
                                                                                                                                                                                               complete sequence of perlecan, a basement membrane heparan ate proteoglycan, reveals extensive similarity with laminin A n, low density lipoprotein-receptor, and the neural cell adhesion
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35; Conserv
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                   (Mouse)
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32, Last sequence update)
42, Last annotation update)
-specific heparan sulfate pr
(HSPG) (Perlecan) (PLC).
                                                                                                                                     PubMed=2972708;
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                                                                                                                                                                                                                                                                                                                                                                                      proteoglycan
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with other basement
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                        for cells
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Pfam; PF00006; EGF; 4.

Pfam; PF00047; ig; 15.

Pfam; PF00052; laminin_EGF; 7.

Pfam; PF00053; laminin_EGF; 7.

Pfam; PF00053; laminin_EGF; 7.

Pfam; PF00053; laminin_EGF; 7.

Pfam; PF00053; laminin_EGF; 7.

Pfam; PF00054; laminin_BG; 3.

Pfam; PF00057; ldl recept_a; 4.

Pfam; PF00057; ldl recept_a; 4.

Pfam; PF00057; Ldl recept_a; 7.

R Pfam; PF00050; SEA; 1.

R PCODm; PD003031; Laminin_B; 3.

R SMART; SM00408; EGF_Lam; 7.

R SMART; SM00201; LamB; 3.

R SMART; SM00201; LamB; 3.

R SMART; SM00202; LDLAG; 3.

R SMART; SM00200; SEA; 1.

R SMART; SM00200; SEA; 1.

R SMART; SM00200; SEA; 1.

R PROSITE; PS00026; EGF_3; 4.

PROSITE; PS00026; EGF_3; 4.

PROSITE; PS00025; LAM G DOMAIN, 3.

R PROSITE; PS01248; LAMININ TYPE_EGF; 11.

R PROSITE; PS01248; LDLRA_2; 4.

R PROSITE; PS01209; LDLRA_1; 4.

R PROSITE; PS01204; SEA; 1.

R PROSITE; PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M77174; AAA39991.1; -.

EMBL; J04054; AAA39992.1; -.

EMBL; J04055; AAA39912.1; -.

PIR; S18252; S18252.

PDB; 1GL4; 28.NOV-01.

MGD; MGI:96257; H8pg2.

GO; GO:0005604; C:basement membrane; IDA.

GO; GO:0005604; C:basement localization; IMP.

InterPro; IPR008985; ConA like_lec_gl.

InterPro; IPR008985; ConA like_lec_gl.

InterPro; IPR000742; EGF 2.

InterPro; IPR000704; IGF 1lke.

InterPro; IPR000704; IGF 1lke.

InterPro; IPR0003598; Ig_C2.

InterPro; IPR000034; Laminin_BGF.

InterPro; IPR000034; Laminin_BGF.

InterPro; IPR0000172; Lominin_GGF.

InterPro; IPR000172; Lominin_G.

InterPro; IPR000082; SEA_domain.

InterPro; IPR000082; SEA_domain.
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SUBCELLULAR LOCATION: Extracellular.

TISSUE SPECIFICITY: Found in the basement membran. TISSUE SPECIFICITY: Found in the basement membran. THEE HEPARAN SULFATE CHAINS AS WELLAND O-LINKED OLIGOSACCHARIDES.

SIMILARITY: Contains 4 LDL-receptor class A domain. SIMILARITY: Contains 11 laminin EGF-like domains.

SIMILARITY: Contains 3 laminin IV domains.

SIMILARITY: Contains 15 immunoglobulin-like C2-ty.

SIMILARITY: Contains 1 EGF-like domains.

SIMILARITY: Contains 1 EGF-like domains.

SIMILARITY: Contains 1 SEA domain.
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een the Swiss Instit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  components such as laminin, prolargin and
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      BASEMENT MEMBRANE-SPEC
SULFATE PROTEOGLYCAN (
SEA.
LDL-RECEPTOR CLASS A :
LDL-RECEPTOR CLASS A :
                                                                MEMBRANE-SPECIFIC HEPARAN
PROTEOGLYCAN CORE PROTEIN.
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IS AS WELL ?
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DO
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IG-LIKE C2-TYPE 1.

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 4 (INCOMPLETE).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 9 (C-TERMINAL).

LAMININ EGF-LIKE 11.

IG-LIKE C2-TYPE 10.

LAMININ EGF-LIKE 11.

IG-LIKE C2-TYPE 14.

IG-LIKE C2-TYPE 15.

IG-LIKE C2-TYPE 15.

IG-LIKE C2-TYPE 13.

IG-LIKE C2-TYPE 14.

IG-LIKE C2-TYPE 15.

LAMININ G-LIKE 3.

LEPARAN SULPATE (POTENTIAL).

MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).

EGF-LIKE C2-TYPE 15.

LAMININ G-LIKE 3.

IG-LIKE C2-TYPE 15.

LAMININ G-LIKE 3.

IG-LIKE C2-TYPE 15.

LAMININ G-LIKE 3.

IG-LIKE C2-TYPE 15.

LEPARAN SULPATE (POTENTIAL).

MEDIATES (POTENTIAL).

MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).

EFFARM SULFATE (POTENTIAL).

MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).

EFFARM SULFATE (POTENTIAL).

EFFARM
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TE (POTENTIAL).
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R NEURON ATTACHMENT
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Matches 94
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P15814;
01-APR-1990
01-APR-1990
15-MAR-2004
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                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Immunoglobulin lambda-like polypeptide i precursor (Immunoglobulin-
related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
(CD179b antigen).
IGLL1 OR IGL1.
                                                                                                                                                                  HUMAN
                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
SEQUENCE FROM N.A.
MEDLINE=89315835; PubMed=2501791;
                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                              VMHEALHNHYTOKSLSLSP-----GLOLDETCAEAQDGELDGLWT
                                                                                                                                                                                                                                                                     YPSDIAVEWESNGOP-ENNYKTTPPVLDSDGSFFLY---SKLTVDKSRWQQGNVFSC--S
                                                                                                                                                                                                                                                                                           VCQVAGSSHPEHEASFKLTVPSSQNSSFRLRSPVISIEPPSSTVQQGQDASFKCLIHEGA
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20.2%;
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Primates;
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Pred. No. (
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                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Strausberg R.D., Felmpold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in pre-B cells and
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TISSUE=Lymphoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McKearn J.P
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                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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Natl. Acad. Sci. U.S.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes 14.1 and 16.1 and e human immunoglobulin
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EMBL; M34511; AAA36096 EMBL; M34512; AAA36096 EMBL; BC01229; AAA1122 PIR; A33911; A33911. HSSP; P01842; 7FAB. Genew; HGNC:5870; IGLI EMBL; M27749; AAA36100.1; -.
EMBL; M34513; AAA36096.1; -.
EMBL; M34511; AAA36096.1; JOINED.
EMBL; M34512; AAA36096.1; JOINED.
EMBL; BC012293; AAH12293.1; -. Pfam; PF00047; ig; i. SMART; SM00407; IGc1; 1 PROSITE; PS50835; IG_LII entities requires a license agreement (S or send an email to license@isb-sib.ch). the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I GO; GO:0016020; C:membrane; NAS. GO; GO:0003793; F:defense/immunity GO; GO:0006955; P:immune response; InterPro; IPR007110; Ig-like. This InterPro; IPR007110; Ig-like. IPR003597; Ig_c1. IPR003006; Ig_MHC. IGLL1. NAS. (See There are no restrictions ong as its content is in . Usage by and for http://www.isb-sib. for .ch/announce, ö

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Best Local :
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21-JUL-1986
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _MOUSE
LAC2_MOU
P01844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiger
SIGNAL
CHAIN
This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                             Azuma T., Steiner L.A., Eisen H.N.; "Identification of a third type of lambda light immunoglobulins", proc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
                                                                                        SEQUENCE OF 66-104 (MOPC 315), AN MEDLINE=81223782; PubMed=6165998;
                                                                                                                           Biochemistry 12:5400-5416(1973).
                                                                                                                                    PHENDLINE=74048693, PubMed=4760498; Dugan E.S., Bradchaw R.A., Simms E.S., "Amino acid sequence of the light chair (MOPC-315).";
                                                                                                                                                                                                          "Somatic variants of murine Nature 298:380-382(1982).
                                                                                                                                                                                                                                                                                                 MEDLINE=82274221; PubMed=6287422; Wu G.E., Govindji N., Hozumi N., Murie "Nucleotide sequence of a chromosomal immunoglobulin gene of mouse.";
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83014953; PubMed=6812053; Selsing E., Miller J., Wilson R., Storb U.; Selsing E., Miller J., Wilson R., Storb U.; Evolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                 immunoglobulin-like domain.
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IMMUNOGLOBULIN LAMBDA-LIKE PO
J REGION (BY SIMILARITY TO LA
LICHT-CHAIN).

C REGION (BY SIMILARITY TO LA
LICHT-CHAIN).
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Pred. No. 0.00
%1; Mismatches
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 a collaboration - MBL outstation -
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RESULT 73
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Best Local :
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DISULFID
SEQUENCE
        InterPro; IPR007110; I
InterPro; IPR003597; I
InterPro; IPR003006; I
InterPro; IPR000353; N
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                         "Class II genes of miniature swine. IV. expression of two allelic class II DQB of Immunol. 145:1946-1951(1990).
                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                          HSSP;
                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         Gustafsson K., Leguern C., Hirsch
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                          precursor
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                                                                                                                                                                                                                                                                                                                                                                                                       P15983;
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P13760; 2SEB.
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104 AA;
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Pred. No. 0.00016;
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Sus.
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Best Local S
Matches 46
                                                                                       axonogenesis.";

J. Neurosci. Res. 42:547-561(1995).

-I- FUNCTION: Cell adhesion molecule with an important role in the development of the nervous system. Involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc. Bit o axonin on neurons (By similarity).

-I- SUBCELULLAR LOCATION: Type I membrane protein.
-I- TISSUE SPECIFICITY: Expressed in postmitotic neurones in 16-36 hour embryos, including those in the brain, cranial ganglia and otic and olfactory placodes, and in all classes of spinal
                                                                                                                                                                                                                                                                                                                                                                                                                               CAM1 BRARE
Q90478;
10-OCT-2003
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DISULFID
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                              MEDLINE=96155762; PubMed=8568941;
Tongiorgi E., Bernhardt R.R., Schu
"Zebrafish neurons express two L1
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                          Tongiorgi E., Bernhardt R.H
"Zebrafish neurons express
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                              Neural cell
NADL1.1.
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15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00299; IG_MIC; 1.
MHC II, Transmembrane; Glycopi
SIGNAL 1 31
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
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DEVELOPMENTAL STAGE: Onset of expression correlates with the initiation of axonogenesis in 16-36 hour embryos. SIMILARITY: Belongs to the immunoglobulin superfamily. L1/neurofascin/NgCAM family. SIMILARITY: Contains 6 immunoglobulin-like C2-type domains. SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
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                                                                                                                                                                                                                                                                                                                                                                          (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
"conton molecule L1.1 (N-CAM L1.1)
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28; MHC_II_beta;
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POT N-LINKED (GLCNAC. CRC64;
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Pred. No. 0.
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EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
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D L1-related
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Best Local S
Matches 94
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Pfam; PF00047; ig; 6.

PFANTS; PR00014; ENTYPEIII.

SMART; SM00060; FN3; 5.

SMART; SM00408; IGC2; 4.

PROSITE; PS50835; IG LIKE; 6.

Neurogenesis; Cell adhesion; Du
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PIR; T30581; T30581.
HSSP; P20241; 1CT8.
ZFIN; ZDB-GENE-980526-512; ni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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InterPro;
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b; IPR003961; FN_III.
c; IPR003962; FnIII subd.
c; IPR007110; Ig-like.
c; IPR003598; Ig_c2.
                                                  LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
                                                                                                                                            HLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSF
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- VDPRRRV - - - SSGKLILSNVEFSDTAVYQCEAVNKHGSILI - - -
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
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Pred. No. 0.0042;
D; Mismatches 18
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CYTOPLASMIC (POTENTIAL).
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p01842; p80423;
p01842; p80423;
21-JUL-1986 (Rel. 01, Creat)
21-JUL-1986 (Rel. 43, Last)
15-MAR-2004 (Rel. 43, Last)
15-JUL-1986 (Rel. 43, Last)
15-JUL-1986 (Rel. 43, Last)
15-JUL-1986 (Rel. 43, Last)
16-JUL-1986 (Rel. 01, Last)
16-JUL-1986 (Rel. 01, Last)
16-JUL-1986 (Rel. 01, Creat)
16-JU
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HUMAN
Ponsting H., Hess M., Hilschmann M., Ponsting H., Hess M., Hilschmann M., Primary structure of a "Structural rule of antibodies. Primary structure of a immunoglobulin-L-chain of the lambda type, subgroup IV recein Kern). V. The complete amino acid sequence and
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=71150336; PubMed=5549568; Ponstingl H., Hess M., Hilschmann
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (BENCE-JONES PROTEIN SH).
MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Put
"The amino acid sequence of a lambda
complete amino acid sequence and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                        SEQUENCE
                                                                                                                                                                                      "Comparative studies on the structure of the light chains immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
                                                                                                                                                                                                                                                                                                    MEDLINE=83186114;
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                                                                                                                                                                                                                                                                                (BENCE-JONES PROTEIN NIG-64).
B3186114; PubMed=6404900;
F., Takayasu T., Suzuki S., S
                                                                                                                                          (BENCE-JONES PROTEIN KERN).
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110:631-652(1968)
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or send a
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MEDLINE=9013913, PubMed=2515285,
Ely K.R., Herron J.N., Harker M.,
"Three-dimensional structure of a
water. Conformational flexibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen B.L., Poljak R.J.;
"Amino acid sequence of the (laminous continuous (IgG New).";
Biochemistry 13:1295-1302(1974)
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                          MEDLINE=82080680; PubMed=6273747;
Hieter P.A., Hollis G.F., Korsmey,
"Clustered arrangement of immunog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2...
Edmundson A.B., Ely K.R.,
Panagiotopoulos N.,
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MEDLINE=75046825; Pubr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The three-dimensional myeloma immunoglobulin
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[5]
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                                                                                                                                                                                                                                                                                                               in man.'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the Mcg lambda Biochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poljak R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stoppini M., Bellotti V., Negri A., "Characterization of the two unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=74109253;
                                                                                                                                                                                                                                                                                                                                                                                             MO1.
                                                                                                                                                                                                   MISCELLANEOUS: The sequence shown is the Kern-/Oz-/Mcg-chain found in proteins SH, X, and NIG-64. The Kern protein has the Kern the NEWN protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker.

MISCELLANEOUS: Six tandem lambda-type genes were identified and the J most 5 were sequenced. These correspond to the Mcg sequence (lambda-1), the Kern-/Oz- sequence (lambda-2) and the Kern-/Oz-
                                                                                                                                                                           sequence (lambda-3).
SIMILARITY: Contains 1 immunoglobulin-like domain.
 J00253;
L38562;
X51754;
X51755;
                                                                non-profit institutions as long as its content
d and this statement is not removed. Usage by ar
s requires a license agreement (See http://www.isb-
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dimensional structure of the fab' fragunoglobulin at 2.0-A resolution.";
Acad. Sci. U.S.A. 71:3440-3444(1974).
AAA59107.1;
AAB36581.1;
CAB38569.1;
CAA36049.1;
                                                                                                                                                                                        (lambda-3).
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PubMed=4215080;
L L.M., Avey H.P., Cl
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GO; GO:0006955; P:immune response; NJ
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGcl; 1.
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PDB; 1LTL; 15-MAY-97.
Genew; HGNC:5855; IGLC1.
Genew; HGNC:5856; IGLC2.
Genew; HGNC:5857; IGLC3.
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Ll adhesion protein 1 precursor (V-CAM 1)
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8; Mismatches 40
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S -> G (IN KERN+ MARKER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR 003901.
R -> K (IN OZ+ MARKER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_003900.
T -> K (IN MCG+ N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE
                                                                                                                          PRT;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Sheamen C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Cybulsky M.I., Fries J.W.U., Williams F
Byers M., Shows T., Gimbrone M.A. Jr.,
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splicing of the human VCAM1 gene.";
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"Crystal structure of an integrin-binding fragment of vascular adhesion molecule-1 at 1.8-A resolution.";
                                                                                                                                                                                                                                                                   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Expainski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieder M.J.,
Rajkumar N.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osborn L., Hession C., Tizard R., Vassallo C., Luhowskyj S., Chi-Rosso G., Lobb R.; Chi-Rosso G., Lobb R.; "Direct expression cloning of vascular cell adhesion molecule 1, cytokine-induced endothelial protein that binds to lymphocytes."; Cell 59:1203-1211(1989).
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MEDLINE=91016951; PubMed=1699207;
MEDLINE=91016951; PubMed=17.V.;
Polte T., Newman M., Gopal T.V.;
"Full length vascular cell adhesion molecule 1 (VCAM-1).";
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=91201302; PubMed=1707873;
Hession C., Tizard R., Vassallo C., Schiffer S.B., Goff
Chi-Rosso G., Luhowskyj S., Lobb R., Osborn L.;
"Cloning of an alternate form of vascular cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90090619; PubMed=2688898; Osborn L., Hession C., Tizard R.,
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                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
                                                                                                                                                                                                                                          Proc.
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, Collins T.;
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EMBL; X53051; CAA37218.1; -. EMBL; M30257; AAA513917.1; ALT_TE EMBL; M73255; AAA61270.1; -. EMBL; M60335; AAA61269.1; -. EMBL; AF536818; AAM96190.1; -. EMBL; BC017276; AAH17276.1; -.
Pfam; PF00047; 1g; 6.
Pfam; PF00047; 1g; 6.
PRINTS; PR01472; ICAMYCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM00408; IGC2; 3.
SMART; SM00408; IGC2; 3.
PROSTTE; PS50835; IG LIKE; 5.
PROSTTE; PS50835; IG LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PDB; 1VSC; 20-JUN-96.
PDB; 11J9; 07-NOV-01.
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Wang J.-H., Stehle T., Pepinsky R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Browning B., Osborn L.;
"The crystal structure of an N-terminal two-domain vascular cell adhesion molecule 1 (VCAM-1): a cyclithe domain 1 C-D loop can inhibit VCAM-1-alpha 4 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang J.-H., Pepins
                                                                                                                                                                                              Genew; HGNC:12663; VCAM1.
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                                                                                                             InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007710; Ig-Tike.
InterPro; IPR00398; Ig c2.
InterPro; IPR003989; VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Structure of a functional fragment of VCAM-1 refined at 1.9-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: By cytokines (e.g. IL-1, TNF-alpha).
PTM: Sialoglycoprotein.
DISEASE: May play an important role in the genesis o:
artherosclerosis and rheumatoid arthritis.
SIMILARITY: Contains 7 immunoglobulin-like C2-type d:
DATABASE: NAME=PROW; NOTE=CD guide CD106 entry;
WMWM="http://www.ncbi.nlm.nih.gov/prow/cd/cd106.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
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B41288; B41288.
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NE=95296382; PubMed=7539925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflamed tissue
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UE SPECIFICITY: Expressed on inflamed vascular endothelium,
as on macrophage-like and dendritic cell types in both nor
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AAA51917.1; ALT_TERM
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IMPORTANT IN CELL-CELL RECOGNITION.
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Liu J.-H., Karpusas
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                                                                                                                                          LALLPAATQGNKV-----VLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILG---NQ
CPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
            APEIFWSKKLDNGNLQHLSGNATLTLIAMRMEDSGIYVCEGVNLIGKNRKEVELIVQ---
                                         LVCRAKLHIDEMDSVPTVRQAVKĖLQVYISPKNTVISVNPSTKLQEGGŠVTMTCSSEGLP
                                                                                                  GTTSTLTMNPVSFGNEHSYLCTATCESRK--LEKGIQVEIYSFPKDPEIHLSGPLEAGKP
                                                                                                               G--SFLTKGPSKLNDR-----ADSRRSLWDQG-----NFP------
                                                                     ITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLETKSLEVTFTPVIEDIGKV
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                           -QCRSPRGKNIQGGKTLSVSQLELQDSGTWTC----TVLQNQKKVEFKIDIVP
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IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 4
IG-LIKE C2-TYPE 6
IG-LIKE C2-TYPE 6
IG-LIKE C2-TYPE 7
                                                                                                                                                       Score 157; DB 1;
Pred. No. 0.0034;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
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CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASCULAR CELL ADHESION PR
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                  FTId=VAR_014311
                                                                                                                                                                                                                                                                                                                              /FTId=VAR_014309
                                                                                                                                                                                                                                                                                    FTId=VAR_014312
                                                                                                                                                                                                                                                                                                                FTId=VAR_014310
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(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; 3D-structure
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                                                                                                                                                                                                                                                                                                                                                                                                                          7654321
                                                                                                                                                                     Length 739;
                                                                                                                                                                                                                                                                                                                                                     Short).
                                                                                                                                                         Indels 158;
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(POTENTIAL).
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RESULT
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10-OCT-2003 (Rel. 42, Last sequence update)
Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (Sirp-alpha-2) (Sirp-alpha-3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based activation motifs) (Bit) (Macrophage fusion receptor) (p84).
PTPNS1 OR SHRPS1 OR SIRP OR MYD1 OR BIT OR MFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHS1 HUMAN (P78324; 000683;
    Deloukas P., Matthews L
Jones M., Stavrides G.,
                                                                                                                    MEDLINE=20053880, PubMed=10585853; Sano S.-I., Ohnishi H., Kubota M.; "Gane structure of mouse BIT/SHPS-1."; Biochem. J. 344:667-675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Monocytes;
MEDLINE=98143722; PubMed=9485180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors.
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                                               MEDLINE=21638749;
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97215901; PubMed=9062191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujioka Y., Kasug
"Mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (amao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocalization of genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386:181-186(1997).
                                                                                                                                                                                                                                                                                  FROM
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GLY-75; ASP-95;
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                                                                                                                                                                                                                                                                                                                          28:1-11(1998).
PubMed=11780052;
hews L.H., Ashurst J., Burton J.,
es G., Almeida J.P., Babbage A.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORM 3),
ND VAL-131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION ND INTERACTIONS WITH PTPN11; PTPN6 AND GRB2
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Primates;
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                                                                                                                                                                                                                                                     AND VARIANTS LEU-44; THR-50; THR-52; LEU-96; ASN-100; ARG-107; GLY-109 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT; 503 AA.
Q8TAL8; Q9H0Z2; Q9UDX2; Q9UIJ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND VARIANTS
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RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Coulson A., G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramssy H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA ROCKETS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RC TISSUE=Brain, Kidney, and Skin;
RX MEDLINE=22388257; pubMed=12477932;
RX MEDLINE=22388257; pubMed=12477932;
RX MEDLINE=22388257; pubMed=12477932;
RX Altusnberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hikesley R.W., Touchman J.W., Green E.J., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
North Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Maliszewski C.,
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"Negative regulation of growth hormone
signal regulatory protein alpha.";
J. Biol. Chem. 275:28222-28229(2000).
                                                                                                                                                                                                                                                                                                                                                                    Schraven
                                                                                     MEDLINE=21400825;
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                      Delespesse G.,
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99401000; PubMed=10469599;
                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, AND INTERACTIONS WITH FYB; SCAP2
                                                                                                                                                                                                                                                                                                                                                                  J.F., Swanson K.D., Marie-Cardine A.,
ven B., Neel B.G.;
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                                                                                                           AND
                                                              Tanaka H.,
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                                                                                                           INTERACTION WITH CD47.
                    Lindberg F
Sarfati M.;
                                                     regulation of
                                        F.P.,
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                                        Oldenborg
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human T
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LEU-96; ASN-100; ARC
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                                            Rubio M.,
Ullrich
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  and
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Bentley D.R., Beck S.,
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                                                                                                                                                                                            Carter-Su
signaling
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                                                                 Brown
                                                                                                                                                                                                                                                           AND JAK2
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Matches
                                        Query Match
                                                                                                                                   EMBL; AB023430; BAA87929.1; -.
EMBL; AC004832; AAF19260.1; -.
EMBL; AL034562; CAB38674.1; -.
EMBL; AL049634; CAB4662.1; ALT_SEQ.
EMBL; AL117335; CAC12723.1; -.
EMBL; BC035692; AAH3692.1; -.
EMBL; BC035692; AAH3692.1; -.
EMBL; BC03592; AAH33092.1; -.
EMBL; BC03591; AAH33510.1; -.
EMBL; BC03591; AAH33510.1; -.
                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells and inhibite cyrokine production by mature dendritic cells. SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPNC. Binds GRB2 in vitro. Binds FGR (By similarity). Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B. SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P78324-3; Sequence=VSP_007029;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
Detected on myeloid cells, but not T cells. Detected at lower levels in heart, placenta, lung, testis, ovary, colon, liver, small intestine, prostate, spleen, kidney, skeletal muscle an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity). Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin. Mediates negative regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Immunoglobulin-like cell surface receptor for CD47. as docking protein and induces translocation of PTPN6, PTPN11
                                                                                GO:0005886; C:plasma membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: N-glycosylated on tyrosine residues in response to PTM: Phosphorylated on tyrosine residues in response to stimulation with EGF, growth hormone, insulin and PDGF. Dephosphorylated by PTPN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and its cognate receptor signal-regulator protein-alpha: -regulation of IL-12 responsiveness and inhibition of dendritic
                                                                                                                                                                                                                                                                                                                 D86043;
Y10375;
Y11047;
                                                                                                     602461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P78324-2; Sequence=VSP_007030; Note=No experimental confirmation av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P78324-1; Sequence=Displayed;
    l Similarity 79; Conserv
                                                                                                                   HGNC:9662; PTPNS1.
  6.5%;
ilarity 24.8%;
Conservative 45
                                                                                                                                                                                                                                                                                                               CAA71944.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                       BAA12974.1;
                                                                                                                                                                                                                                                                                                                                       CAA71403
; Score 156.5; DB 1;
; Pred. No. 0.0022;
45; Mismatches 153;
                                                                                TAS
                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage by
                                      Length 503;
    Indels
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  41;
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  Gaps
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136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVL-QNQKKVE 194

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RESULT 78
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Best Local
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21-JUL-1986 (Rel. 01, Last /
21-JUL-1986 (Rel. 42, Last
10-OCT-2003 (Rel. 42, Last
                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01846;
                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02129; L1PG.
HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulins.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: This chain was obtained from a mixture of normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=78000254; PubMed=409425;
Novotny J., Franek F., Margolies M.N.,
"Amino acid sequence of normal (microh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAC_PIG
                                                                                                                                                                                                                                                                                                                                                                                      NIEMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunoglobulin lambda chains
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                                                385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
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                                                                                                                                                                                                                             Similarity
                     SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                LK-VSAHPKEQGSNTAAE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FK----SGAGTELSVRAKPSAP-VVSGPAARATP-----
SNNKYAASSYLALSASDWKSSSGFTCQVTHE
                                                                                                                                                QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHVTLQGDPLRGTANLSETIRVPPTLEV-TQQPVRAE---NQVNVTCQVRKFYPQRLQLT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D--ITLKWFKNGNELSDFQTNVDPVGESVSYSIHSTAKVVLTREDVHSQVI-----CEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPARELIYNQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGSPDTE 132
                                                                                                                                                                                                                                                                                                        104
105 AA;
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01, Created)
01, Last sequence up
42, Last annotation
                                                                                                                                                                                                                                                                                                        104 J
11003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Ig-like.
; Ig_cl.
; Ig_MHC.
                                                                                                                                                                                                                           6.5%;
35.2%;
                                                                                                                                                                                                   15;
                                                                                                                                                                                                                        Score 156; DB 1;
Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE
                                                                                                                                                                                                                                                                                                        3817AAEBD747C396
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91
                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                   Length 105
                                                                                                                                                                                                                                                                                                        CRC64;
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RESULT 79
LAC5_MUSSP
ID LAC5_M
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                    LAC RABIT P01847;
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                                                                          21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Ig lambda chain C region.
SEQUENCE
                                    Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mami F., Cazenave P.A., Kindt T.J.; "Conservation of the immunoglobulin C lambda 5 EMBO J. 7:117-122(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig lambda-5 chain C region.
Mus spretus (Western wild mouse).
                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin
NON TER 1
DOMAIN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35582; AAA39152.1; -. HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=88196070; PubMed=3129289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P20765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                       TNNKYMVSSYLTLISDQWMPHSRYSCRVTHE---GNTVEKSVS 100
                                                                                                                                                                                                                                                 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                           QPKSDPLVTLFLPSLKNLQANKVTLVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQPSKQ
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27
104
105
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                                                                                                                                                                                                                                                                                                                                               6.4%; Score 153.5; DB 1; 34.0%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                         11674 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin C
                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (WITH HEAVY CHAIN).; AAB417DF68471A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE
                                                                                                                                                  PRT;
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RESULT 81
KACB_RABIT
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986
21-JUL-1986
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                 KACB_RAE
P01839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      Heidmann O., Rougeon F.;
"Multiplicity of constant kappa light chain
genome: a b4b4 homozygous rabbit contains a
EMBO J. 2:437-441(1983).
                                                                                                                                                                                                                                                                                                          Oryctolague cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE_NEG
          EMBL; V01241; CAA24558.1;
EMBL; V00885; -; NOT_ANNO
                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia I. Jaton J.-C.; "The primary structure of the constant region of Basilea-rabbit immunoglobulin lambda-chains."; Biochem. J. 197:177-183(1981).
                                                                                                                                                                                                                                                       STRAIN=Basilea;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                    K-BAS
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                                                                                                                                                                                                                                                                                                                                                            Ig kappa-B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specificity.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                  MISCELLANEOUS: In Basilea rabbits, the major type of light is lambda. The kappa chain shown is a minor component. All rabbit B allotypes have Cys-64.
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: This lambda chain expresses
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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105
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(Rel.
(Rel.
Chain
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ilarity 32.7%;
Conservative 17
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01, Last sequence update)
43, Last annotation updat
C region.
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Pred. No. 0.00054;
7; Mismatches 45
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B427513272E8663D CRC64;
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kappa-bas ger
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Matches 31
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P01880;
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SMART; SM00407; IGC1; 1.

PROSITE; PS50835; IG_LIKE; 1.

PROSITE; PS00290; IG_MHC; FALSE_NEG.
MEDLINE=81133632;
                                                                                                          MEDLINE=81199406; PubMed=6785754;
Shinoda T., Takahashi N., Takayas
                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 158-383 (MYELOMA PROTEIN WAH).
MEDLINE-81223768; PubMed-6787589;
Lin L.-C., Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-162 (MYELOMA PROTEIN WAH).

MEDLINE=82082419: PubMed=6947220;

Putnam F.W., Takahashi N., Tetaert D., Debuire B.,

Panino acid sequence of the first constant region of 
hinge region of the delta heavy chain of human IgD 
proc. Natl. Acad. Sci. U.S.A. 78:6168-6172(1981).
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGHD.
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21-JUL-1986 (Rel. 01,
10-OCT-2003 (Rel. 42,
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InterPro; IPR003597;
InterPro; IPR003006;
                   CARBOHYDRATE-LINKAGE
                                                                                                                                                                                                 "Amino acid sequence of galactopamine-containing hinge region of a human immunoglobulin D.";
                                                                                                                                                                                                                                                                                           SEQUENCE OF 103-137
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                                                                                       "Complete amino
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                                                                                                                                                                                                                                                                                                                   L.-C., Putnam F.W.; Imary structure of the Fc region of human immunoglobulin lications for evolutionary origin and biological function or. Natl. Acad. Sci. U.S.A. 78:504-508(1981).
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31; Conser
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                                                                                                                                              158-383
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llarity 33.7%;
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                                                                                       acid
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PubMed=7008791;
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Ig_cl.
Ig_MHC.
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Pred. No. 0.00
19; Mismatches
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                       Takahashi
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c region
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CRC64;
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SSERRERSSS

KACA RAT

STANDARD;

106

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PO1836;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
21-JUL-1986 (Rel. 42, Last annotation up
3 Ig kappa chain C region, A allele.
3 Rattus norvegicus (Rat).
5 Rattus norvegicus (Rat).
6 Eukaryota, Metazoa; Chordata; Craniata;

update) on update)

Eukaryota; Metazoa; Mammalia; Eutheria;

Craniata; Vertebrata; F Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Rat

Rattus

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RESULT 83
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Matches 58
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GO; GO:0006955; P:immune re
InterPro; IPR007110; Ig-lik
InterPro; IPR003597; Ig_c1:
InterPro; IPR003006; Ig_MHC
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NON TER 1

DOWAIN 6

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DOWAIN 267

DISULFID 15

DISULFID 161

DISULFID 161
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:5480; IGHD.
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                                                                                                                                                    292
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                                                                                                                                                                                                             Similarity
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                                 TLNHPSL
                                                  SVMHEAL
                                                                                  CLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                                                                                                                                    STPLQQWRQG-EYKCVVQHTASKSKKEIFRWPESPKAQASSVPTAQPQAEGSLAKATTAP
                                                                                                                                                  TVLHQDWLNGKEYKCKVSN------
                                                                                                                                                                   PKD-----NSPVVLACLI-TGYHPTSVTVTWYM-GTQSQPQRTFPEIQRRDSYYMTSSQL
                                                                 CFVVGSDLKDAHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNAGTSVTC
                                                                                                  ATTRNTGRGGEEKKKEKEKEEQEERETKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFT
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383
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                                  256
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42125
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373
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1331
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; Ig_c1.
; Ig_MHC.
                                                                                                                  EKTISKAKGQPREPQ-------VYTLPPSRDEL-TKNQVSLT
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                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin
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                                                                                                                                                                                                                                   O-LINKED.
O-LINKED (POTENTIAL).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
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O-LINKED.
O-LINKED.
O-LINKED.
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Pred. No. 0.0035;
2; Mismatches 8
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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Best Local S
Matches 29
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HSSP; P01842; 2MCG;
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                             HB2C_PIG
P15982;
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       PIG
          EMBL; M31497; AAA31084.1; -. EMBL; M32117; AAA53110.1; -. PIR; A60404; A60404.
                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                           "Class II genes of miniature swine. IV. Characterization expression of two allelic class II DQB cDNA clones."; J. Immunol. 145:1946-1951(1990).
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90361905; PubMed=2391424;
                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ h
                                                                                                                                                                                                  Sache D.
                                                                                                                                                                                                            Gustafsson K.,
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    Sue scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=82082587; PubMed=6273908;
Sheppard H.W., Gutman G.A.;
"Allelic forms of rat kappa chain genes: evidence
selection at the level of nucleotide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
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PROSITE; PS00290; IG_MHC; 1.

    !- SIMILARITY: Contains 1 immunoglobulin-like domain

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Pred. No. 0.
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FJ:
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                                                                                                                                                                                                              Germana S.,
                                                                       noved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
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KILO_RAT
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AC Q9Z0J
DT 30-MB
DT 10-OC
DE Kilor
OS Rattu
OC Eukar
OC Mamma
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Matches 56
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Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC III beta; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00209; IG MHC; 1.
MHC II; Transmembrane; Glycoproteir
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DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                    anchored present family.";
                                                                                                                                                                                                                                                                                                                                                                            KILO_RAT STANDARD; PRT; 348 AA 920018; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last amotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
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TRANSMEM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last annotation update) Kilon protein precursor (Kindred of IgLON)
                                                                                                                                                     Funatsu N., Miyata S., Kumanogoh Sokawa Y., Maekawa S.;
                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                 MEDLINE=99175207; PubMed=10075727;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000353; MHC_II_beta.
                                                                                                           "Characterization of a novel rat brain glycosylphosphatidylinositol-
nchored protein (Kilon), a member of the IgLON cell adhesion molecu
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N-AA9581F2A3B1969D C
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EXTRACELLULAR BETA-2.
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SMART; SM00408; IGc2; 2.
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SIMILARITY: Belong
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Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abd
subcutaneous fat biopsy: kappa IV immunoglobulin
Biochem. Biophys. Res. Commun. 245:713-716(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=81042304; PubMed=6775818;

Hitter P.A., Max E.E., Seidman J.G., Maizel J.V.

"Cloned human and mouse kappa immunoglobulin consigenes conserve homology in functional segments."

Cell 22:197-207(1980).
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MEDLINE=72188439; PubMed=5027703;

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Suter L., Barnikol H.U. Matanabe S., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";

the mechanism of antibody production.";

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                                                  TISSUE=Abdominal adipose tissue;
MEDLINE=98249779; PubMed=9588180;
                                                                                                                                                                                                                                                                                                                                                                                                       Hilschmann N., Barnikol H.U., Hess M., Steinmetz-Kayne M., Suter L., Watanabe (In) France F., Shugar D. (eds.); Gamma globulins: structure and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gottlieb P.D., Cunningham B.A., Rut "The covalent structure of a human acid sequence of the light chain.";
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IGKC.
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Gall W.E., Edelman G.M.;
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Intrachain disulfide bonds.";
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MEDLINE=71064023; PubMed=5489770;
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Mammalia; Eutheria; Primates;
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Ig kappa chain C region.
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nan gamma G-immunoglobulin.
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PDB; 1D5B; 09-FEB-00.

PDB; 1D5I; 09-FEB-00.

PDB; 1D5I; 04-CCT-00.

PDB; 11FZ; 08-JUL-03.

PDB; 11FZ; 08-JUG-01.

PDB; 11FZ; 108-JUG-01.

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EMBL; V00557;
PIR; B90562; K
PDB; 1D5B; 09-
                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
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15-MAR-2004 (Rel. 43, Last ann
Neurofascin precursor.
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SMART; SM00407; 1Gc1; 1.
PROSITE; PS50855; 1G LIKE; 1.
PROSITE; PS00290; 1G_MHC; 1.
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                                                                                          Archosauria; Aves;
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                          Neognathae;
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86
106
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V -> L (IN INV(1,2) MARKER)
/FTId=VAR 003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
E -> Q (IN REF. 5 AND 6).
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Pred. No. 0.00
Pred. No. 0.00
                                                                                      Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae.
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"Organization of the neurofascin gene and analysis of developmentally regulated alternative splicing,";
J. Biol. Chem. 272:28742-28749(1997).
-I- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis, myelination and neuron-glial cell interactions (By similarity).
-I- SUBCELIULAR LOCATION: Type I membrane protein.
-I- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2), SEQUENCE OF 758-781 AND 801-815, CLEAVAGE AT ARG-636, AN TISSUE-Brain; MEDLINE-92317154; PubMed=1377696; Volkmer H., Hassel B., Wolff J.M., Frank R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superfamily.";
J. Cell Biol. 118:149-161(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=Brain;
WEDLINE=92317154; PubMed=1377696;
WOlkmer H., Hassel B., Wolff J.M., Frank R.,
"Structure of the axonal surface recognition
"Structure of the axonal subgroup of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: There is one major 'emultiple 'late' isoforms. Around 50 isoform different developmental stages.

PTM: N-glycosylated and O-glycosylated.

PTM: May be proteolytically cleaved at Arg SIMILARITY: Belongs to the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L1/neurofascin/NgCAM family.
SIMILARITY: Contains 5 fibronectin type III domains.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2; Comment=A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=042414-2; Sequence=VSP_008935, VSP_008936;
VELOPMENTAL STAGE: There is one major 'early' isoform and
iltiple 'late' isoforms. Around 50 isoforms are found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=042414-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rathjen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.G., Volkmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DF 26-46; 637-641; 717-730; AND GLYCOSYLATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rathjen F.G.;
molecule neurofascin
immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily.
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EMBL; X65224; CAA46330.1; -.
EMBL; Y13431; CAA74726.1; JOINED.
EMBL; Y13432; CAA74726.1; JOINED.
EMBL; Y1343; CAA74726.1; JOINED.
EMBL; Y13434; CAA74726.1; JOINED.
EMBL; Y13435; CAA74726.1; JOINED.
EMBL; Y1351; CAA74726.1; JOINED.
EMBL; Y1352; CAA74726.1; JOINED.
EMBL; Y1352; CAA74726.1; JOINED.
EMBL; Y1353; CAA74726.1; JOINED.
EMBL; Y1354; CAA74726.1; JOINED. SMART; SN PROSITE; Cell adhe Pfam; PF00041; fn3; 5. Pfam; PF00047; ig; 6. SMART; SM00060; FN3; 5. Interpro; IPR003961; FN III. InterPro; IPR008957; FN III-like. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2. SM00408; IGC2; 3. E; PS50835; IG_LIKE; Repeat; Signal; Transmembrane; Immunoglobulin domain;

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244
                               189
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                                                                                                                             49
                                                                                                                                             12
                                                                                                                                                                                    Similarity
               QKNPYTLK---VKTKKPHNETSLRNHTDMYSARGVTETTPS-FMYPYGTSSSQMVLRGVD
                              NOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG----
                                                              PPGSSPSV-----QCRSP--RGKNIQGGKT--LSVSQLELQDSGT-WTCT-----VLQ
                                                                              RNDYGTALSSKIHLQVSRSPLW-----PKEKVDVI-----EVDEGAPLSLQCNP
                                                                                               N-----
                                                                                                                             IQFHWKNSNQIKILGNQGSF--LTKGPSKLNDRADSRRSLWD------QGNFPLII
                                                                                                                                            GIAFALCLHHLISAIEVPLDSNIQSELPQPPTITKQSVKDYIVDPRDNIFIECEAKGNPV
                                                                                                                                                            GVPF----RHLLLVLQLAL-----LP----AATQGNKVVLGKKGDTVELTCTASQKKS
-- VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
                                               PPGLPPPVIFWMSSSMEPIHQDKRVSQGQNGDLYFSNVMLQDAQTDYSCNARFHFTHTIQ
                                                                                                             PTFSWTRN-----GKFFNVAKDP-KVSMRRRSGTLVIDFHGGGRPDDYEGEYQCFA
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                                                                                        -LKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
                                                                                                                                                                            63;
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 111 1.

FIBRONECTIN TYPE-II1 2.

FIBRONECTIN TYPE-II1 3.

FIBRONECTIN TYPE-II1 4.

FIBRONECTIN TYPE-III 4.
                                                                                                                                                                                                           MW;
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N-LINKED
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                                                                                                                                                                                    Score 148;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                          N-LINKED (GLCNAC
                                                                                                                                                                                                                                                   SCLSSPV -> F
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                  /FTId=VSP_008935.
Missing (in isoform 2).
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                            835F27D086B2BFF6 CRC64;
                                                                                                                                                                                                                                                                                         (GLCNAC.
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                                                                                                                                                                                    DB 1; Length 1369; .029;
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                                                                                                                                                                           182;
                                                                                                                                                                                                                                                  isoform
                               PSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                           Indels 128;
                                                                                                                                                                                                                                                                                        (POTENTIAL)
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell add
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q13449;
01-NOV-1997
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associated membrane protein (LAMP).";
Gene 170:189-195(1996).

-i- FUNCTION: MEDIATIES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).
                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                                                                                                                                                                                         MIM; 603241; -.
GO; GO:0007399; P:neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U41901;
PIR; JC4776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96235133; PubMed=8666243;
Pimenta A.F., Fischer I., Levitt P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Limbic system-associated membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tracts as well as in single layers of the superior colliculus, spinal chord and cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:6705; LSAMP.
                                                                                                                                                                                                                   Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLECIASGV----PAPDIMWYKKGGELPAGKTK--LENFNKALRISNVSEE--
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                                                                                                                                                                                                                Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belongs to the immunoglobulin superfamily. IgLON
    338
122
214
304
111
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 institutions as long as its content
LIMBIC SYSTEM-ASSOC PROTEIN.

REMOVED IN MATURE FIG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                         adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                    SYSTEM-ASSOCIATED MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338
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                                                                                                                        FORM
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                                                                                                                                                                                                                                           GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LSAMP)
                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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RT "Expression patterns of L1-family cell recognition molecules L1, CHL1, RT "Expression patterns of L1-family cell recognition molecules L1, CHL1, RT NrCAM, and neurofascin in the mouse brain.";

RT NrCAM, and neurofascin in the mouse brain.";

RT NrCAM, and neurofascin in the mouse brain.";

RT NrCAM, and neurofascin, in the mouse brain which may be completed in neurofascin, and protein which may be involved in neurite extension, anomal guidance, synaptogenesis, cc involved in neurofascin, axonal guidance, synaptogenesis, cc myelination and neuron-glial cell interactions (By similarity).

CC -1- SUBUNIT: Probable constituent of a neurofascin/NRCAM/ankyrin G complex. Associates with the sodium channel beta-1 (SCNIB) and CC complex. Associates with the sodium channel beta-1 (SCNIB) and CC complex. Associates with the sodium channel beta-1 (SCNIB) and CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.

CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                              NFAS MOUSE
Q810U3;
15-MAR-2004
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CARBOHYD
                                                                                                                                                                                                             STRAIN-Swiss Webster;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                      Neurorascin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA---KTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGHD-----KWSLDPRVELEKRHSL----EYSLRIQKVDVYDEGSYTCSVQTQHEPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PAPDFEWYRDDTRINSANGLEIKSTEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPP-TITESKSNEAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EVOLLVEG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGNQGSFLTKGPSKLNDRA---DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
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                                                                                                                                                                                                                                                                                                                                 (Rel. 43, Created)
(Rel. 43, Last seq
(Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                      precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VTNVTEEHYGN---YTCVAANK 295
                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                             TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                   sequence update) annotation updat
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Pred. No. 0.0059;
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                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                  CHL1
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Best Local S
Matches 100
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Pfam; PF00047; ig; 6.

SMART; SM00060; FN3; 4.

SMART; SM00409; IG; 6.

SMART; SM00408; IGc2; 6.

PROSITE; PS50835; IG LIKE; 6.
                                                                                                                                                                                    CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_L.
Cell adhesion; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ543322; CAD65849.1; -. MGD; MGI:2442229; D430023G06Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro;
151
                   127
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                                                                                                                                                      Similarity
PSVQCRSPRGKNIQGGKTLS-----VSQLELQDSGT-WTCTVLQN-----QKKVEFK 196
                   ALSNRIRLQVSKSPLW----PKENLDPVV--
                                                           NPAPSFHWTRNSRFFNIAKDPRVSMRRRSGTLVIDFRSGGRPEEY-EGEYQCFARNKFGT
                                                                              KKSIOFHW-KNSNOIKILGNOGSFLTK--GPSKLNDRADSRRSLWDQGNFPLIIKN----
                                                                                                    PWVHIALILFILSIGGAIEIPMDPSIQNELTQPPTITKQSVKDHIVDPRDNILIECEAKG
                                                                                                                       PERHLLIVIQUALLPAA-----
                                     -----LKIEDSDTYICEVEDQKBEVQLLVFGLTANSDTHLLQGQSLTLTLESPPG-SS
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IPR007110; Ig-like.
IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003961; FN_III.
IPR008957; FN_III-like.
                                                                                                                                                                                                                  162
268
358
358
353
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446
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483
7783
                                                                                                                                           Conservative
                                                                                                                                                                                    AΑ;
                                                                                                                                                                                                                                                                                                                                           924
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1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                     6.18;
                                                                                                                                                                                     137975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal;
                                                                                                                                            66;
                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                     FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 2
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
                                                                                                                                           Score 147; DB Pred. No. 0.03
                                                                                                                                                                                                                                     N-LINKED
N-LINKED
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROFASCIN.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
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(GLCNAC.
(GLCNAC.
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                                                                                                                       -----TOGNKVVLGKKGDTVELTCTASO
                                                                                                                                                      .03;
                   -----VQEGAPLTLQCNPPPGLPS
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                                                                                                                                                             1;
                                                                                                                                             183;
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                                                                                                                                                              Length 1240;
                                                                                                                                            Indels 118;
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(POTENTIAL).
                                                                                                                                           Gaps
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RESULT 90
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                                                                                                                              Query Match
Best Local :
                                                                                                      Matches
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NON TER 1
DOMAIN 6
                                                                                                                                                                                                                                                                                                                        Přám; Přó0047; ig; 1.
Přám; Přó0047; IGcl; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Immuno;
                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig lambda-1 chain C region.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87305594; PubMed=3114047; Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two genes and a single V lambda gene."; Gene 55:75-84(1987).
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M22520; AAA41419.1; ALT_INIT.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/
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QPKATPSVTLFPPSSEELKTDKATLVCMVTDFYPGVMTVVWKADGTPITQGVETTQP-FK 59
                                                QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
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                                                                                                 Score 146; DB
Pred. No. 0.00
19; Mismatches
                                                                                                                                                                                                                               INTERCHAIN (WITH HEAVY CHAIN).
                                                                                                                                                                                                                                                                                  IG-LIKE
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Pfam; PF00047; 19; 6.

SMART; SM00060; FN3; 4.

SMART; SM00408; IGC2; 5.

PROSITE; PS50835; IG_LIKE; 6.

Neurogenesis; Cell adhesion; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAML_RAT
Q05695;
01-FEB-1994
 TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence up
15-MR-2004 (Rel. 43, Last annotation
Neural cell adhesion molecule L1 precu
L1CAM OR CAML1.
                                                                                                                                                                                                                                                                                                                                         L1/neurofascin/NgCAM family.
-!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                   DOMAIN
                                                        SIGNAL
                                                                   Alternative
                                                                                                                                                           InterPro; IPR003961;
InterPro; IPR007110;
InterPro; IPR003598;
                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                    PIR; S36126; S36126.
                                                                                                                                                                                                                              EMBL; X59149; CAA41860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                             Transmembrane; Repeat; Immunoglobulin
                                                                                                                                                                                 interPro,
                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                          Name=2; Synonyms=Llcs;

IsoId=Q05695-2; Sequence=VSP_002592;

TISSUE SPECIFICITY: Isoform 2 is predominantly found in the while isoform 1 is found in the peripheral nervous system similarity: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q05695-1; Sequence=Displayed;
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                                                                   splicing.
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                                                                                                                                                        ; FN_III-like.
; FN_III.
; Ig-like.
; Ig_c2.
                                                                                                     <u>ب</u>
                                                                             Developmental protein;
oglobulin domain; Signal
EXTRACELLULAR (POTENTIA:
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE 1.
                                           BY SIMILARITY.
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                                             ADHESION MOLECULE
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                                                                             Signal;
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                                                                                          Glycoprotein
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                                                                                                                                                                                                                       GLTAN-----SDTHLLQGQSLTLTLESPPGSSPSVQCRSP-----RGKNIQGGKTL
                                                                                                                                                                                                                                                         ------DLQERGDSDKYFIEDGQ--LVIKSLDYSDQGDYSCVASTELDEVESRAQLLVV
                                                                                                                                                                                                                                                                                                             ILANLQVKEATQITQGPRSTIEKKGARVTFTCQASFDPSLQASITWRGDGR------
                        R--EPQV---YT----LPPSRDELTKNQVSLTCLVKGFYPSDIA 363
                                                                           S---TYRVVSVLTVLHQDWLN-GKEYKCK-
                                                                                                                           LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK---FNWYVDGVEVHNAKTKP-REEQYN
                                                                                                                                                                             SVSQLELQDSGTWTCTVLQNQKKVE--FKIDIVPCPAP-EPKSCDKTHTCPELLGGPSVF
                                                                                                                                                                                                        GSPGPVPHLELSDRHLLKQSQVHLSW-----SPAEDHNSPIEKYDIEFEDKEMAPEKWF
                                                                                                                                                                                                                                                                                  FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLVF
KGPEPQVTIGYSGEDYPQVSPELEDITIFN-SSTVLVR-WRPVDLA
                                                   APQIQYRV----
                                                                                                                                                      SLGKV----PGNQTSTTLKLSPYVHYTFRVTAINKYGPGEPSPVSETVVTPE-----
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                     -----AAPEKN--PVDVRGEGNETNNMVITW------
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                                                   ----QWRPLGKQETWKEQTVSDPFLVVSNTSTFVPYEIKVQAVNNQG
                                                                                                                                                                                                                                                                                                                                                               43;
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
PIBRONECTIN TYPE-III 1
PIBRONECTIN TYPE-III 2
PIBRONECTIN TYPE-III 3
CELL ATTACHMENT SITE (
CELL ATTACHMENT SITE (
CELL ATTACHMENT SITE (
BY SIMILARITY,
BY SI
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Pred. No. 0
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W; 0F12A7C4415F3C08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT

92

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LAC_CHICK
ID LAC_CHICK
AC POTES
AC POTE
                       RESULT 93

KACE RAT

ID — KACE RAT

STANDARD; PRT; 106 AA.

AC P01835;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 19 Kappa chain C region, B allele.

OS Rattus norvegicus (Rat).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratt
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Best Local S
Matches 29
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10-OCT-2003 (Rel. 4
Ig lambda chain C r
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SMART; SM00407; IGc1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87218480; PubMed=3107981; Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.; "Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus."; EMBO J. 6:97-102(1987).
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PIR; B26167; B26167.
NCBI_TaxID=10116;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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Pred. No. 0.0017;
9; Mismatches 39;
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77BF341B511B91B2 CRC64;
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STRAIN=Oregon-R;
MEDLINE=89028670; PubMed=3141062;
Seeger M.A., Haffley L., Kaufman T.C.;
Seeger M.A., Haffley L., Kaufman T.C.;
Characterization of amalgam: a member superfamily from Drosophila.";
Cell 55:589-600(1988).
                                                                                                                                                                                              Amalgam protein precursor.

AMA OR BG:DS00276.6 OR CG2198.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheppard H.W., Gutman G.A.; "Allelic forms of rat kappa chain genes: evidence selection at the level of nucleotide sequence."; Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                                                                                                                                                                                                                                                           P15364; Q9V3A5;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
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SMART; SM00407; IGc1; 1
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HSSP; P01842; 2MCG.
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-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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PROSITE; PS00290; IG_MHC; 1.
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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D -> N (IN REF. 2).
N -> K (IN REF. 2).
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V -> VW (IN REF. 2).
S -> N (IN REF. 2).
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RA Beeson K.Y., Benor P.V., Bernan B.P., Bhandari D., Bolbakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Cawley S., Gelbart W.M., Classer K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stagleton M., Strong R., Sun E.,
RA Yellams S.M., Moodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
RA Yelson C., Turner R., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R. M., Wyers B.W., Rubin G.M., Venter J.C.,
The Genome Sequence of Drosophila melanogaster.";
                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=2242606; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Ch
George R.A., Guarin H., Kronmiller B., Pacleb J.M.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length CDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
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Celniker S.E., Pfeiffer B.D., Knafels J.,
Palazzolo M.J.;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                        - I - SUBCELLULAR LOCATION: Attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132
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                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
AE001572; AAD19797.1;
                        M23561; AAA28367.1;
                                                                                                                                                                                                                                                                                                                                                                        ដ
                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                        the membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C., Champe M.,
b J.M., Park S., Wan K.H.,
                                                                                                                                                                                                                                                                                                                                                                        by a GPI-anchor
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RESULT 95
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SIGNAL
                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular cell adhesion protein 1 precursor (V-CAM VCAM1 OR VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 3.

SMART; SM00408; IGc2; 2.

SMART; SM00408; IG LIKE;

PROSITE; PS50835; IG LIKE;
SEQUENCE FROM N.A. (ISO)
STRAIN=FVB; TISSUE=Lung
MEDLINE=92181437; PubMeo
                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                             P29533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0000071; Ama.
GO; GO:0005886; C:plasma membrane;
InterPro; IPR007110; Ig-11/Re.
InterPro; IPR003598; Ig_c2.
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PIR; A31923; A31923
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AY051911; AAK93335.1;
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                                                                                                                                                                                                                                 VDGVEVHNAKTKPREEQYNSTYRVVSVL---TVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                  NAVMPAGGHLLAEPTLRIRSVHRMDRGGYYC-IAQNGEGQPDKRLIRVEVEFRPQIA---
                                                                                                                                                                                                                                                                                                                       QCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN-----QKKVEFKIDIVPCP
                                                                                                                                                                                                                                                                                                                                             QVLVSATEKVTKKLSLQIKTPPVIAENTPKSTLVTEGQNLELTCHANGFPKPTISWAREH
                                                                                                                                                                                                                                                                                                                                                                                       VVLSMRNILSLPDQRYNVTVTEGPKT------GSAIYTFRIQNIEVSDMGPYEC
                                                                                                                                                                                                                                                                                                                                                                                                                                   LIFCLAISLDSVLSAPVISQISKDVVASVGDSVEFNCTVEEVGQLSVSWAKRPSESDTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLVLQLAL-----LPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-----KNSNQ
                                                                                                                                                                                                                                                                            APEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                 EV-----EDOKEEVQLL---VFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----
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                                                                                                                                                                                                             KNGVPLQSSRHHEVANTASSSGTTTSVLRIDSVGEEDF---GDYYCNATNK
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333
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                                                                            (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; Glycoprotein; Membrane; GPI-anchor; Signal;
                                                                                                                                                       STANDARD;
 PubMed=1371918;
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                     (ISOFORM 1).
                                                    Chordata;
Rodentia;
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REMOVED IN MATURE F
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
Q -> K (IN REF. 1).
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Pred. No. 0.0086;
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                                                     Craniata; Vert
Sciurognathi;
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                                                     Vertebrata; Euteleostomi;
hi; Muridae; Murinae; Mus
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(POTENTIAL)
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TISSUB-Lymph node;
MEDLINE-93246254; PubMed=
Araki M., Araki K., Vassa
"Cloning and sequencing o
Gene 126:261-264(1993).
                                                                                                                                                                                                                                                                                                                                                    STRAIN=FVB/N; TISSUB=Kidney;
MEDLINE=93317595; PubMed=7687058;
Terry R.W., Kwee L., Levine J.F., Labow M.A.;
"Cytokine induction of an alternatively spliced murine adhesion molecule (VCAM) mRNA encoding a glycosylphosphatidylinositol-anchored VCAM protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:5919-5923(1993).
                                                                                                                                                                                                                  Korenaga R., Ando J., Tsuboi H., Kamiya A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION

-IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1

INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL

TRANSDUCTION. THE VCAM1/VLA4 INTERACTION MAY PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FVB; TISSUE=Lung;
MEDLINE=93232042; PubMed=7682556;
Moy P., Lobb R., Tizard R., Olson D., Hession C.;
"Cloning of an inflammation-specific phosphatidyl i
form of murine vascular cell adhesion molecule-1.";
J. Biol. Chem. 268:8835-8841(1993).
                                                <del>-</del>
                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NIH Swiss, and 129/Sv;
Kumar A.G., Dai Y.X., Kozak C.A., Mims M.P.,
Ballantyne C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hession C., Moy P., T. Burkly L., Miyake K., "Cloning of murine and Biochem. Biophys. Res
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                                                                                                                                                                                                                                                                                                            TISSUE=Endothelial cells;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 311-345 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kumar A.G., Dai
Ballantyne C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95015899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-693 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 18:387-391(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cybulsky M.I., Allan-Motamed M., Col
"Structure of the murine VCAM1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94117008; PubMed=7507076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine VCAM-1. Molecular cloning,
IsoId=P29533-2; Sequence=VSP_002581, VSP_002582; TISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, well as on macrophage-like and dendritic cell types in both nor and inflamed tissue.

PTM: The GPI-anchor is located on position 319 of isoform 2.
                                                                                                                                        PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES EMIGRATION TO SITES OF INFLAMMATION. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (SHORT ALTERNATIVE PRODUCTS:
                                                                              Name=2; Synonyms=Short;
                                                                                                                          Event=Alternative splicing; Named
                                                                                           ime=1; Synonyms=Long;
IsoId=P29533-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C., Moy P., Tizard R., Chisholm P., Williams C., Wysk M. Myake K., Kincade P., Lobb R.; of murine and rat vascular cell adhesion molecule-1.", Biophys. Res. Commun. 183:163-169(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153:4088-4098(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7523515;
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This

SIMILARITY: Contains 7 immunoglobulin-like C2-type

domains.

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EMBL; M84487; EMBL; L22353; EMBL; L22350; EMBL; L22350; EMBL; L22353; EMBL; L22353; EMBL; L22350; EMBL; L22350; EMBL; L22350; EMBL; L22350; EMBL; L22369; EMBL; U12878; EMBL; U12878; EMBL; U12871; EMBL; U12873; EM
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DOMAIN
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PRINTS; PR01472; ICAMYCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM004008; IGc2; 3.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain; Glycoprotein;
                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:98926; Vcam1.
GO; GO:0007155; P:cell adhesion;
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003899; VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B48919; A46052.
PIR; JN0581; JN0581.
HSSP; P19320; 1VCA.
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                                                                                                                                                                                                                                                                                                                   GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed.
       AAA40546.1;
AAA64832.1;
AAC37607.1;
AAB88576.1;
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AAA80012.1;
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AAB60660.
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                               Alternative splicing
                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                                                                 VASCULAR CELL
                                                                                                                                                                                                                                                                                                                                  Cell adhesion;
                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                               ADHESION PROTEIN
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                                                                                                                                                                                                                                                                                                                                    Transmembrane;
     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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RESULT 96

LAMP RAT

ID LAMP RAT

AC 0628T3;

DT 01-NOV-1997 (
DT 10-OCT-2003 (
DE Limbic system
GN LSAMP OR LAMP
OS RATTUS NOV-699

OC Mammalia; But
OX NCBI TAXID=10

RN [1] TAXID=10

RN [1] TAXID=10

RN SEQUENCE FROM
RC TISSUE-Hippoc

RX HENZEL M., F.,
RA HENZEL M., F.,
RA HENZEL W., F.,
RA HENZEL W.,
RA HENZEL W., F.,
RA HENZEL W.,
RA HENZEL W., F.,
RA HENZEL W.,
RA HENZEL W., F.,
RA HENZEL W.,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
    Pimenta A.F., Zhukareva V., Barbe M.F., Henzel W., Fischer I., Levitt P.; "The limbic system—associated membrane pmember that mediates selective neuronal Neuron 15:287-297(1995).

-i- FUNCTION: MEDIATES SELECTIVE NEURONACONTRIBUTES TO THE GUIDANCE OF DEVELORMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                         SEQUENCE FROM N.A.,
TISSUE=Hippocampus;
MEDLINE=95374785; Processor & Thirty
                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                  LSAMP OR LAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                      system-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVLTCAAIGCDSPSFSWRTQTDSPLNGVVRNEGAKSTLVLSSVGFEDEHSYLCAVTCLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKGDTVELTCTASQKKSIQFHW--KNSNQI-KILGNQGSFLTKGPSKLNDRADSRRSLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEGINEA---GISRKSVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSDGIPAPKIL--WSRQLNNGELQ-----PLSEN----TTLTFMSTKRDDSGIYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVKGFYPSDIAVEWE----SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP-PSRDELTKNQVSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPNVYPFDHLEIELLKGETTLMKKYFLEEMGIKSLETKILETTFIPTIEDTGKSLVCLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVDV---SHEDPE-----VKFNWYVDGVEVHNAKTKPREEQY----NSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLEKRTQV-----EVYSFPEDPVIKMSGPLVHGRPVTVNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP----KDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTLTLESPPGSSPSVQCRSPRGKNIQG-----GKTLSVSQLELQDSGTWTCTVLQNQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGNATLTLIAMRMEDSGVYVCEGVNLIGRDKAEVELVVQEKPFIVDISPGSQVAAQVGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGNFPLIIKNLKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEGGAVIMICSSEGLPAPEIFWGRKLDNEVLQLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693
739
                                                                                                                                                                                                                                                                                                                                                       (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
531
561
310
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                               PubMed=7646886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·EMESEPKQRQSVQPLYVNVA----PKETTIWVSPSPILEE--GSPVNLTC
                                                                                                                                                                                                                                                    ; Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531
561
345
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                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%;
19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81317
    SELECTIVE NEURONAL GROWTH AND AXON TARGETING GUIDANCE OF DEVELOPING AXONS AND REMODELING
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                      membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Μ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 002581.
/FTId=VSP 002581.
Missing (In isoform :
/FTId=VSP 002582.
D -> N (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (i
/FTId=VSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 144.5;
Pred. No. 0.0
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
EKPFIVDISPGSQVAAQVGDSVVLTCAAIGCDSPSF
GRMKSQITNGHQLTVHLMFAKSFYFICYLCLYLAL (
                                                                                                                                                                                                                                                Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D2134C341E5E449
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                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           338
                                                              protein
l growth
                                                                                                                            Reinoso
                                                                                                                                                                                                                                                      Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .023;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                    precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                is an Ig
                                                                                                                            B.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 123;
                                                                                                                                                                                                                                                      Euteleostomi;
Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                      (LSAMP)
                                                                                                                            Grimley
                                                              superfamily targeting."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739;
                                                                                                                            <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534
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Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; 1g; 3.
SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U31554; AAA86120.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                       GIGID
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH OOF THE HYPPOCAMPAL MOSSY FIBER PROJECTION.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic-
associated cortical and subcortical regions that function in
cognition, emotion, memory, and learning.

DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS
DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE
THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN
HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                   117
   182
                                                                                                                                    73
                                                                                                                                                                 62
                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Lipoprotein.
                                                                                                                                                                                                  LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNS-KVAWLNRSGIIF
                                 LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
                                                                                                                                                               LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
                                                                                                                                                                                                                                  LLLVLQLALLPAA----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
 LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPP-TITESKSNEAT
                                                                  SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEY
                                                                                                 -EVOLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-
                                                                                                                                                                                                                                                                                                                                     338
                                                                                                                                                                                                                                                                                                                                                                      316
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through their extracellular immunoglobulin-like domain.";

RI J. Cell Biol. 154:427-434(2001).

CC -!- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis, compelination and neuron-glial cell interactions. Isoforms 2/3 may be responsible for mediating and signaling axon-glial interaction cluming the early stages of myelination.

C -!- SUBUNIT: probable constituent of a neurofascin/NRCAM/ankyrin G complex. Associates with the sodium channel beta-1 (SCN1B) and conscipring axons as early as postanatal day 5, during the period conscipring axons as early as postanatal day 5, during the period conscipring axons as early as postanatal day 5, during the period conscipring axons as early as postanatal day 5, during the period conscipring axons as early as postanatal day 5, during the period conscipring axonal proteins in close association with CNTNNAP1.

C -I- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2/3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glia
                                                                                                                                                                                                                                                                                                                                                                                  Tait S., Gunn-Moore F., Collinson J.M., Huang J., Lubetzki C. Pedraza L., Sherman D.L., Colman D.R., Brophy P.J.;
"An oligodendrocyte cell adhesion molecule at the site of ass the paranodal axo-glial junction.";
J. Cell Biol. 150:657-666(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION OF ISOFORMS 1 AND 2/3, INDIRECT PHOSPHORYLATION, AND TISSUE SPECIFICITY. MEDLINE=20391985; PubMed=10931875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION OF ISOFORM 2/3.

MEDLINE=90220650; PubMed=9562181;

Collinson J.M., Marshall D., Gillespie C.S., Brophy P.J.;

"Transient expression of neurofascin by oligodendrocytes at the onset of myelinogenesis: implications for mechanisms of axon-glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFAS RAT
P97685; P97684;
15-MAR-2004 (Re
                                                                                                                                                                                                                                                                                       MEDLINE=21363577; PubMed=11470829; Ratcliffe C.F., Westenbroek R.E., Curtis "Sodium channel betal and beta3 subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davis J.Q., Lambert S., Bennett V.; "Molecular composition of the node of Ranvier: identification of ankyrin-binding cell adhesion molecules neurofascin (mucin+/third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tait
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last ann
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Cell Biol. 135:1355-1367(1996).
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the EMBL/GenBank/DDBJ databases
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Sciurognathi; Muridae; Murinae; Rattus.
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InterPro; IPR003967; FN III-like.

InterPro; IPR007101; Ig-like.

InterPro; IPR007104; Ig-like.

InterPro; IPR003788; Ig_c2.

Pfam; PF00041; fn3; 4.

Pfam; PF00047; ig, 6.

SMART; SM00060; FN3; 3.

SMART; SM000408; IGC2; 4.

PROSITE; PS50835; IG_LIKE; 6.

PROSITE; PS50835; IG_LIKE; 6.

PROSITE; PS50835; IG_LIKE; 6.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
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EMBL; U81035; AAB47753.1; -.
EMBL; U81036; AAB47754.1; -.
HSSP; P20241; 1CFB.
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SIMILARITY: Belongs to the immunoglobulin superfamily.
Ll/neurofascin/NgCAM family.
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IsoId=P97685-2; Sequence=VSP_050416, VSP_050417, VSP_050418,
VSP_050419;
Name=3; Synonyms=NF155, 155 kba isoform;
IsoId=P97685-3; Sequence=VSP_050416, VSP_050417, VSP_008941,
VSP_050418, VSP_050419;
TISSUE SPECIFICITY; Isoform 1 is expressed at Nodes of Ranvier
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PTM: Isoform 2/3 is phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  while isoform 2/3 is expressed in unmyelinated axons. DEVELOPMENTAL STAGE: Strongly but transiently up-regulated i oligodendrocytes at the onset of myelinogenesis. Once these have engaged their target exons, expression declines
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Name=1; Synonyms=NF186, 186 kDa isof
IsoId=P97685-1; Sequence=Displayed
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
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FIBRONECTIN TYPE-III 1.
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                                                                      QPENNYKTTPPVLDSD--GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL--
                                                                                                                                                                       DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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/FTId=VSP 050418.
Missing (In isoform 2 a.
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E -> Q (IN REF. 2).
W -> L (IN REF. 2).
Q -> D (IN REF. 2).
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SEQUENCE FROM N.A.

MEDLINE-82059477; PubMed-6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
"Complete sequence of an immunoglobulin and the dideoxynucleotide method of RNA Nucleic Acids Res. 9:4485-4494(1981).
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      MEDLINE=88329081; PubMed=3138116; de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.; "Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-811915; PubMed-6262318;
Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleortide sequence of a 5.5-kilobase DNA segment containing mouse kappa immunoglobulin J and C region genes.";
"I Biol. Chem. 256:5116-5120(1981).
                                         EMBL; V00807; CAA24189.1;
PIR; B90262; KIMS.
PDB; 1AIF; 01-FEB-97.
                                                                                                                                                                                                                                                                                                                                                                  Altenburger W., Neumaier P.S., Stei "DNA sequence of the constant gene kappa chain", Nucleic Acids Res. 9:971-981(1981).
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MEDLINE=81198949; PubMed=6785724;
Altenburger W., Neumaier P.S., Steinmetz M.,
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PDB;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete amino acid sequence of a mouse kappa light chain."; Biochem. J. 128:427-444(1972).
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Svasti J., Milstein C.;
                                                                                                                                                                                                                                                            phosphatase.
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SIMILARITY: Contains
 1FSK;
1KB5;
1KCR;
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ain C region.
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Contains 1 immunoglobulin-like domain.
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Rodentia;
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EMBL; X12875;
PIR; S05479;
                                                              entities requires a license agreement (See or send an email to license@isb-sib.ch).
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-I- FUNCTION: Cell adhesion molecule with an important role development of the nervous system. Involved in neuron-ne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00407; IGc1; 1.
SROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
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SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 5 fibronectin type III domains.
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1KCU; 11-MAY-02.
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rPro; IPR007110; Ig-like.
rPro; IPR003597; Ig_cl.
rPro; IPR003006; Ig_MHC.
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adhesion molecule L1 precursor (N
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MGD; MGI:96721; Llcam.
GO; GO:0007441; P:axon guidance; IV
InterPro; IPR008957; FN III-like.
InterPro; IPR003954; FN III.
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Pred. No. 0.057
53; Mismatches
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FIBRONECTIN TYPE-III 3
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        Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., ARICHARDS S., Woodergen K.J., Mang M.A., Schaefer C.F., Bhat N.K., Wang J., Hsieh F., Wang Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Wang L., Wang J., Hsieh F., Wang J., Hsieh F., Wang J., Hsieh F., Wang J., Hong L., Schmetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schmetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Casrninci P., Prange C., Wang S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Wang R.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ak Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Wallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Gremn E.D., Dickson M.C., Rodriguez A.C., Grimmord T. Schmutz J. Moore B.M.
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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w for large proteins in vitro."; DNA Res. 5:277-286(1998).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                       SEQUENCE OF :
TISSUE=Brain,
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SEQUENCE OF 804-1240
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NFASC OR KIAA0756.
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
The Generation and initial analysis of more than 15,000 full-length
the human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
C.-i- FUNCTION: Cell adhesion, ankyrin-binding protein which may be
the involved in neurite extension, axonal guidance, synaptogenesis,
myelination and neuron-glial cell interactions (By similarity).
C.-i- SUBUNIT: Probable constituent of a neurofascin/NRCAM/ankyrin G
complex. Associates with the sodium channel beta-1 (SCNIB) and
beta-3 (SCN3B) subunits (By similarity).
C.-i- SUBCELLULAR LOCATION: Type I membrane protein.
C.-i- ALTERNATIVE PRODUCTS:
    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                         Pfam; PF00041; fn3; 3.—
Pfam; PF00047; fq; 6.
SMART; SM00060; FN3; 3.
SMART; SM00409; IG; 6.
SMART; SM00408; IGc2; 6.
SMART; SM00408; IGc2; 6.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst. the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commenties requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                      CHAIN
DOMAIN
                                                                                                                                                                                                                                    Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK027553; BAB55195.1; -.
EMBL; AK090639; -; NOT ANNOTATED CDS.
EMBL; AK127424; -; NOT ANNOTATED CDS.
EMBL; BA018299; BAA34476 2; -.
EMBL; BC008124; AAH08124.2; -.
HSSP; P20241; ICFB.
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003961; FN_III-like.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note=No experimental confirmation available;
SIMILARITY: Belongs to the immunoglobulin superfamily.
L1/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 4 fibronectin type III domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=094856-3; Sequence=VSP_008939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=094856-1; Sequence=Displayed;
                                                                                                                                                                                                                                                     Alternative
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POTENTIAL.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

THR-RICH.
                                                                                                                                                                                                   NEUROFASCIN.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                 LECIASGV----PTPDIAWYKKGGDLPSDKAK--FENFNKALRITNVSEE-----DSGE
                                                                                                                                 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
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HGYLLANAFVSVLDVPPRMLSPRNQL
                   HNHYTQKSL----
                                      KP-TVQWMVNGEP---LQSAPPNPNREVAGDTIIFRDTQISSRA----
                                                        SDIAVEWESNGQPENNYKTTPPVLDSD--GSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
                                                                            YFCLASNKM--GSIRHTISVRVKAAÞYWLDEPKNLILAPGEDG-----RLVCRANG-NP
                                                                                            YKCKVSNKALPAPIEKTIS-KAKGQP----REPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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Pred. No. 0.061;
4; Mismatches 176;
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/FTId=VSP 008940.

T -> M (in dbsNP:3795564).

/FTId=VAR 017251.

F -> L (IN REF. 1; BAB55195)
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/FTId=VSP_008939.
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/FTId=VSP_008937.
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/FTId=VSP_008938.
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Search completed: August

2004, 13:09:06

time

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Maximum Match 100%
Listing first 125 summaries
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X Strausberg R.L., Feingold E.A., Wagner L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Scheetz T.E.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Barownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Holards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

A Holton J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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01-0CT-2003 (TrEMBLrel. 2

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Mammalia; Eutheria;
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Homo sapiens
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Catarrhini; Hominidae;
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Q9vnp2 drosophila
Q24273 drosophila
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Q99jc1 mus
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Best Local
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 TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H
Pobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL
EMBL; BX538118; CAD98026.1; -.
Hypothetical protein.
SEQUENCE 482 AA; 52852 MW; E
                                                                                                                                                                                  Q7Z351;
Q7Z351;
01-OCT-2003
01-OCT-2003
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                                                                                                                                                            Hypothetical protein DKFZP686N02209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2003) to the EMBL; BC053984; AAH53984.1; Hypothetical protein. SEQUENCE 470 AA; 51204 MM
                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                  Homo sapiens
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"Generation and initial analysis
and mouse cDNA sequences";
proc. Natl. Acad. Sci. U.S.A. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=9606;
                                                                                      SEQUENCE
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                                                                                      FROM N.A.
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1 protein DKFZp686N02209.
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                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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59.3%;
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                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SIRVGDAAVYYC-----ARGAGRWAPLGAFDIWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1273; DB 4;
Pred. No. 4.2e-98;
                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Similarity

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WEDLINE=2238257; PubMed=12477932;

WEDLINE=2238257; PubMed=12477932;

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Altochul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altochenko L., Marusina K., Former A.A., Rubin G.M., Hong L.,

Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altochenko L., Marusina K., Farmer A.A., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Altochen M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Altochen M.J., Guellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Altochen B.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Altochen B.J., McKernan K.J., Lu X., Gibbs R.A.,

Altochen B.J., McKernan K.J., Lu X., Gibbs R.A.,

Altochen B.J., Wales S., Sanchez A.,

Altochen B., Young A.C., Shevchenko Y., Bouffard G.G.,

Altochen M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Brak Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 279
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Q7Z7P5;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Primates;
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Last sequence update)
Last annotation update)
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Pred. No. 4.8e-97;
9; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 274
                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    Q8NF17;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2003) to the
EMBL; BC051328; AAH51328.1;
        "The nucleotide
                           SEQUENCE FROM
TISSUE=Spleen;
                                                                                                                                                              Q8NF17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                  FLJ00385
                                                                                                             FLJ00385
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                                                                                                                                                                                                                                                                                                                                                                                                                     DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHK
                                                                                                                                                                                                               SLSPG
                                                                                                                                                                                                                                                        ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                  ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                                                                                      VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                                                                                                                                                                               PSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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                                                                                                                                                                                                                                                                                              KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KTLSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein.
469 AA; 5
                    Takano
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                                                                                                                                                               PRELIMINARY;
                                       N.A.
                                                                                                                                                                                                                                   431
         sequence
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                  Ū,
                                                                    Chordata;
Primates;
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         Kikuno R.,
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Pred. No. 1.2e.
34; Mismatches
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                                                                                                                                          Created)
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        R., Nagase
long cDNA
                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
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         T., Ohara O.;
clone isolated
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                                                                               Euteleostomi;
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          from
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          human
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Matches 262
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InterPro; IPR003597; Ig-cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000407; Ig; 3.
SMART; SM00407; IGcl; 3.
SMOSTTE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_MHC; 2.
NON TER
1
SEQUENCE 509 AA; 56111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      Q96P08 PRELIMINARY; PRT; 679 AA.
Q96P08;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pactor VII active site mutant immunoconjugate.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae;
                                                                                                                                          MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.;
"Targeting tissue factor on tumor ocells for immunotherapy in mouse mure of the color of the col
   SEQUENCE FROM N.A. Hu Z., Garen A.; Submitted (FEB-200
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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262; Conserv
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       cen A.;
(FEB-2003)
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509 AA; 56111 MW;
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          ç
                                                                                                                                          or on tumor vascular endothelial cells and by in mouse models of prostatic cancer."; U.S.A. 98:12180-12185(2001).
          the
          EMBL/GenBank/DDBJ databases
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RMBL; Arz,...

R GO; GO:0005576; C:extractory

R GO; GO:0005509; F:calcium ion binomy,

R GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEF

DR InterPro; IPR000152; Asx hydroxyl S.

InterPro; IPR009003; Cys_Ser_trypsin.
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Best Local S
Matches 228
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PRINTS; PRO010; GLABLOOD.

PRINTS; PRO001; GLABLOOD.

SMART; SM00181; EGF; CA; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00069; GLA; 1.

SMART; SM00060; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00116; ASX HYDRXYL; 1.

PROSITE; PS00118; EGF_C; 1.

PROSITE; PS00118; EGF_CA; 1.

PROSITE; PS00118; EGF_CA; 1.

PROSITE; PS0011; GLU_CARBOXYLATION; 1.

PROSITE; PS0035; IG_MEC; 1.

PROSITE; PS00240; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

SEQUENCE 679 AA; 75552 MW; 0B0023AE
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Pfam; PF000009; EGF; 2.
Pfam; PF000594; gla; 1.
Pfam; PF00047; ig; 2.
Pfam; PF00089; trypsin; 1.
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InterPro; IPR006209; I
InterPro; IPR002383; C
InterPro; IPR006210; I
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InterPro; IPR003597; 1
InterPro; IPR003006; 1
InterPro; IPR001254; I
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InterPro; IPR001314;
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                    NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                        APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                          DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                              DPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                      APIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN
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Pred. No. 7.4e
1; Mismatches
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Best Local S
Matches 261
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Strausberg R.;

Submitted (JUN-2002) to the EMB Submitted (JUN-2003) 78.17...

PIR; A60764; A60764.

InterPro; IPR0031710; Ig-like.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003596; Ig_v.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Igc1; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_MHC; 2.
     Q86TT2 PRELIMINARY; PRT; 354 AA. Q86TT2; Q86TT2; Q1-JUN-2003 (TrEMBLrel. 24, Created) Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update) Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update) Human full-length CDNA clone CS0DIO19YF20 of placent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 521 AA;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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(Fragment)
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                                                                                                                                 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
                                                                                                                                                                                                                                              VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILRDDSKNSVHLQMN-----SLKTDDTAVYYC-VRDLEG-----AGKYDWYFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVQPGGSLRLSCAASGFIVSDHYVEWVRQAPGKGPEWVGCFRSKAHKSTTEYAASVKGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLND------
                                                                                                                                                                               KNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQ
                                                                                                                                                                                                                                                                                VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNST
                                                                                                                                                                                                                                                                                                                                TCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPS
                                                                                                                                                                                                                                                                                                                                                                                VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTH
                                                                                                                                                                                                                                                                                                                                                                                                     ----QLELQDSG-----TWTCTV-----LQNQKKVEFKIDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                WGRGILVTVSSASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                                                                                                                                                                                  FRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2AC7D22E72D6CAA2 CRC64;
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        placenta
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           of,
           Homo
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RESULT 8
Q8TC63
ID Q8TC
AC Q8TC
DT 01-J
DT 01-J
DT 01-O
DE Hypo
OS Homo
OC Euka
OC Mamm
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Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITISUE=Placenta;
Li W.B., Gruber C., Jessee J., Polaye.
Li W.B., Gruber C., Jessee J., Polaye.
Full-length cDNA libraries and norma
Submitted (FEB-2003) to the EMBL/GenB
EMBL; BX248278; CAD62606.1; -
GO; GO:0046821; C.Extrachromosomal DN
InterPro; IPR003597; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
                                                         OBTC63; PRELIMINARY;
OBTC63;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Che
Mammalla; Eutheria; Pri
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid.
NON TER
SEQUENCE
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PROSITE;
Plasmid.
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SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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Submitted (FEB-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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232; Conserv
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                                                                                                                                                                               MHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                            LVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
                                                                                                                                                                                                                                                                           VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
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                                                                                                                                                                                                                                                                                                                                                                        SGTWTCTVLQNQKKVEFKIDIVPCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDQG-----NFPLIIKNLKIED-----SDTYICEVE-----
                                                                                                                                                                    MHEALHNRFTQKSLSLSPG
                                                                                                                                                                                                                LVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV
                                                                                                                                                                                                                                                             VLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC
                                                                                                                                                                                                                                                                                                            KDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLT
                                                                                                                                                                                                                                                                                                                                                                                                       K-----TPLGDTTHTCPRCPEPKSCDTPP---PCPRCPEPK----------
                                                                                                                                                                                                                                                                                                                                                                                                                               QLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AA;
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              Chordata;
Primates;
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and normalization
EMBL/GenBank/DDBJ
                                                            Last sequence up
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Pred. No. 1.6e.
25; Mismatches
                                                                                   Created)
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              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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on update)
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databases.
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RESULT
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Q95M34
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Best Local S
Matches 262
                                                                                095M34 PREDITION OF THE PROPERTY OF THE PROPER
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SMART; SM00406; IGv; 1.

PROSITE; PS00196; COPPER BLUE;

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 3.
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EMBL, BC025985, AAH25985.1; -
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activit
GO; GO:0006118; P:electron transport; IEA.
Interpro; IPR000923; BlueCu_1.
Equus caballus (Horse)
Eukaryota; Metazoa; Ch
                                                                  Immunogobulin IGHC1.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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262; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSNTKVDKRVESKYG-PPCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LQNQXKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPXPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GH-----LVMGFGA----HWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSS--PSVQCRSPRGKNI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGKGLEWIGTINFSGN-MYYSPS-LRSRVTMSADM-SENSFYLKLDSVTAADTAVYYCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
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473 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                               472
   Chordata;
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53.7%;
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                                                                                                 Created)

Last sequence update)

Last annotation update)

chain constant region (
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1151; DB 4;
   Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SC----PAPEFLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7e-88;
   Vertebrata;
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   Euteleostomi;
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RESULT
Q7TMK1
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Pfam; PF00047; iGc1; 2.

SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                       Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Roo
   SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUB-Breast tumor;
MEDLINE-22388257, PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.;
Klausner R.D., Collins F.S., Wagner L., S.
Altschul S.F., Zeeberg B., Buetow K.H., S
                                                                                                                                                                                                                                                                                                                                                                                                         Q7TMK1;
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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EMBL; AJ300675; CAC44624.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leibold W., Radbruch
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179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLTSGVHTFPSV-----LOSSGFYSLSSMVTVPASTWTSETYICNVVHAAS--NFK
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nilarity 59.1%;
Conservative 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336
                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                            25,
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                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence that the control of the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 912;
Pred. No. 4.
                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470
             Shenmen C.M., Schaefer C.F.,
                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6e-68;
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                                            Derge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richards
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e J.G.,
Schuler G.D.
Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 11
Q9R1A4
ID Q9R1A
AC Q9R1A
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M3
DT 01-M3
DT 01-M3
DT 01-M4
DT 0
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Best Local Simi
Matches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

roc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                    Q9R1A4;
Q9R1A4;
01-MAY-2000 (
01-MAY-2000 (
01-OCT-2003 (
Gammal heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2003) to the 
EMBL; BC055910; AAH55910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 470 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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    musculus (Mouse)
                                                                                                                                                                                                                                                      434
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                                                                                                                                                                                                                                                                                                                                      374
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                                                                                                                                                                                                                                                  TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                          LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGNILGGPSVF1FPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSATTTAPSVYPLVPGCGDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVDKSSSTAYMELNSLTSEDSAVYYC-----ARYYYSGSYWYFD---VWGAGTTVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSYNQKFKGKATL
                                                                                                                                                                                                                                                                                                                                                                                                                  PREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGFYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----SCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SVSQLELQDSGTW----TCTVLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I PPPREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKL
                                                            (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                PRELIMINARY;
                                      chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51727 MW;
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    13, Created)
    13, Last sequence up
    1. 25, Last annotation
    Mab7 (Fragment).

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                                      (Fragment).
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Pred. No. 1
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                                                                                                                                              437
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                                                            update)
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RESULT 12
Q8R3V9
ID Q8R3V
AC Q8R3V
DT 01-JU
DT 01-JU
DT 01-OC
DE HYDOL
GN IGH-4
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Q8R3V9;
01-JUN-2002
01-JUN-2002
01-OCT-2003
Hypothetical IGH-4.
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Query Match
Best Local S
Matches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

NON TER

1

NON TER

437

437
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PIR; B45837; B45837.
PDB; 1CQK; 11-SEP-99.
PDB; 1191; 25-DEC-02.
PDB; 1KCU; 11-MAY-02.
MGD; MGI:96446; Igh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003056; Ig_V.
Defam. DE700477; G: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister r
antibody (Mab 7, its light and heavy chains) and constru
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y Match 35.9%;
Local Similarity 41.6%;
                                      400
                                                                               345
                                                                                                                                                                 285
                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 LGKKGDTVELTCTAS--OKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
                                                                                                                RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                 ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE
                                                                                                                                                                                                                                                                                                                                                                                                          AAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DOGNEPLI KNIKI EDSDTYI CEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTDSVKGRFTIY
SNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPG
                                                                                                                                                                                                                                                                       LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                 DLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGC-KPCIC----TVPEV
                                                                                                                                                                                                                                                                                                                                                           ELQ-----DSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPGSSPSVQCRSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDKDRNILSLQMSSLRSEDTAMYYC---
                                                                               KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437
437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 867.5; DB 11;
Pred. No. 3.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lah A.K.M., Misra S.;
anti-white pine blister rust
heavy chains) and construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 123;
436
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

21, 21, 25,

Created)
Last sequence update)
Last annotation update)

protein

PRELIMINARY;

469 AA

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Q99LC AC Q99LC AC Q99LC AC Q99LC DT 01-JU DT 01-OC DE Simil GN MUSH MOC ENKAR OC MAmma OC NCBI RP SEQUE
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;

Strausberg R.;

Submitted (MAR-2002) to the EMB Submitted (MAR-2004)

EMBL; BC024405; AAH24405.1; -.

PIR; B45837; B45837.

MGD; MGI:96446; Igh-4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_WHC.

InterPro; IPR00396; Ig_V.

Pfam; PF00047; Ig; 3.

SMART; SM00406; IGV; 1.

PROSITE; PS50035; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 469 AA; 51976 MW;
                                                              O99IC4 PKELLIA.....
O99IC4;
O99IC4;
O99IC4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TREMBLREN CDNA 1810060009 gene.
             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
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 FROM
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                                                                                                                                                                                                                         FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                     FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                         EPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
                                                                                                                                                                                                                                                                                                                               HTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPK
                                                                                                                                                                                                                                                                                                                                           HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKTL-SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGQSLTLTLESPPGSSPSVQCRSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIS-RDNSQSILYLQMN-----ALRAEDSATYYC-ARDRRSSYYY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVQPGGSLRLSCAASGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRF
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 N.A
                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.6%; Score 858.5; 41.6%; Pred. No. 2.
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                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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InterPro; InterPro;

IPR007110; IPR003006; IPR003596;

Ig-like. Ig_MHC. Ig_v.

SEQUENCE FROM N.A. Strausberg R.; Submitted (FEB-2001)

EMBL; BC003878; AAH03878.1; PDB; 2AP2; 24-NOV-99.

to the

EMBL/GenBank/DDBJ

databases

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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DR RP SEE PRODUCT OF THE PRODUCT OF 
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Best Local Sim
Matches 191;
                                                                                                                                                                                                      Q99L31 PRELIMINARY; PRT; 468 AA.

C Q99L31;

C Q99L31;

T 01-JUN-2001 (TrEMBLrel. 17, Created)

T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Similar to RIKEN CDNA 1810060009 gene.

S Mus musculus (Mouse).

S Mus musculus (Mouse).

C EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; El

C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; N

C NCBI TaxID=10090;
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Pfam; PF00047; ig; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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MGD; MGI:96446; Igh-4
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40.6%;
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Pred. No. 1.5e-62;
3; Mismatches 111;
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REDIENCE FROM N.A.

CSTRAINCS78L/63; TISSUE=Pancreas;

CSTRAINCS78L/63; TISSUE=Pancreas;

X MEDLINE=21085660; PubMed=11217851;

XX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XX Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

XX A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XX A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XX A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XX Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XX A Fleischmann W., Gansterland T., Gissi C., King B., Kochiwa H.,

XX A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XX A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XX A Schriml L.M., Staubli F., Suzuki R., Tomita M., Barsh G.,

XX A Schriml L.M., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

XX Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

XX A Brownstein M.J., Bult C., Fletcher C., Fujita M., Geriboldi M.,

XX Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

XX Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 198
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                    Q9D8L4;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 468 AA; S1661 MW;
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IGH-1 OR 1810060009RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKATITADTSSNTAY-LQLSSLTSEDTAIYYC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTISKPKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEP
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Last sequence update)
Last annotation update)
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Pred. No. 2.4e-62;
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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     Lee N.H.,
lerts P.,
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SEQUENCE FROM N.A. Strausberg R.; Submitted (FEB-200

(FEB-2001)

6 the

EMBL/GenBank/DDBJ

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;

Craniata; Vertebrata; E Sciurognathi; Muridae;

Euteleostomi; ; Murinae; Mus

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RESULT 16
Q99L2
ID Q99L2
AC Q99L2
DT 01-JU
DT 01-JU
DT 01-OC
DE Simil
OS Mus m
OC Eukar
OC Mamma
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Best Local S
Matches 185
                                                                                                                                                                                        Q99L25 PRELIMINARY; PRT;
Q99L25; O1-JUN-2001 (TrEMBLrel. 17, Create
O1-JUN-2001 (TrEMBLrel. 17, Last so
O1-CCT-2003 (TrEMBLrel. 25, Last and
Similar to RIKEN CDNA 1810066009 go
Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 4.
PROSITE; P8500290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK007918; BAB25349.1;
PIR; S26746; S26746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSY
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Pred. No. 2.8e-
67; Mismatches
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Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databa
REMBL; BC010327; AAH10327.1; -.
R MGD; MG1:2144967; AU044919.
R GO; GO:0005489; F:electron transporter activity; IE/
R GO; GO:0006118; F:electron transport; IEA.
R InterPro; IPR000346; CyrC heme_BS.
R InterPro; IPR007110; Ig-1Ike.
R InterPro; IPR007110; Ig-1Ike.
InterPro; IPR00306; Ig_MHC.
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Best Local S
Matches 193
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 52449 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91Z05;
Q91Z05;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090; [1]
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical AU044919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SVSQLELQ------DSGTW-----TCTVLQ--NQKKVEFKID-----IVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --WGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS
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41.2%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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19,
25,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Sim
Matches 188;
         GO; GO:0005489; F:electron transporter ac GO; GO:0006118; P:electron transport; IEA InterPro; IPR003045; CytC heme_BS. InterPro; IPR007110; Ig-like. InterPro; IPR007106; Ig-MHC. InterPro; IPR003066; Ig_wC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                      Q8R3H6;
Q8R3H6;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; BC025447; AAH25447.1; -.
MGD; MGI:2144967; AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00190; CYTOCHROME
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG-MHC; 1.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW;
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090;
                                                                                                                                                                                                                  Hypothetical AU044919.
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                      Mus musculus (Mouse)
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SMART; SM00406; IGv;
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                                                                                                                                                FROM N.A.
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Pred. No. 2.8e-59;
1; Mismatches 127
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Sciurognathi; Muridae;
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Best Local S
Matches 193
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01-JUL-1997
01-JUL-1997
01-OCT-2003
                                                                    SEQUENCE FROM N.A.

MEDLINE=98017879; PubMed=9379478;

MEDLINE=98017879; PubMed=9379478;

Fomegaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Fomegaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4

their respective simian immunodeficiency virus genes.";

J. Med. Primatol. 26:120-128(1997).

EMBL; AF0011225; AAB60872.1;

EMBL; P01730; 1WIQ.

HSSP; P01730; 1WIQ.
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Mammalia; Eutheria; Primates; C
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=60711;
                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecus sabaeus
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SEQUENCE 4:
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GO:0016020; C:membrane; IEA.
GO:0006955; P:immune response;
erPro; IPR000973; CD4_TCAg.
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Last annotation update)
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Pred. No. 3.4e-
63; Mismatches
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Matches 148; Conserv
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O09262;
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGV;
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NCBI_TaxID=60712;
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Pfam; PF00047; Ig; 2.

PRINTS; PR00692; CD4TCANTIGEN

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HSSP; P01730; 1WIQ.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:1mmune response; IEA.
GO; GO:0006955; P:1mmune TCAg.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
Pf6m; PF00047; ig; 2.
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NCBI_TaxID=60712;
  Cercopithecus pygerythrus.
Eukaryota; Metazoa; Chordata;
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Pred. No. 8.1e-56;
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Craniata; Vertebrata; Euteleostomi;
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                   EMBL; AF001223; AAB60870.1; -.
HSSP; P01730; IWIQ.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; I
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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01-JUL-1997
01-OCT-2003
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                                                                                                                                    SEQUENCE FROM N.A. PubMed=9379478;
MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey"
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SMART; S
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NCBI_TaxID=60711;
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MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C.,
                                                                                                               their respective simian immunodeficiency J. Med. Primatol. 26:120-128(1997).
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                                                                                                                                                                                                                                                                                             CD4 (Fragment).
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 PRINTS;
             Pfam; PF00047;
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nes 148; Conserv
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3; SM00406; IGv; 1.
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Pred. No. 8.1e-56;
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Best Local S
Matches 147
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HSSP; P01730; 1WIQ
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; II
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig-V
Pfam; PF00047; Ig; 2.
PRINTS; PR00699; CD4TCANTIGEN.
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MEDLINE-98017879; PubMed-9379478;

MEDLINE-98017879; PubMed-9379478;

Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Norther S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.";

J. Med. Primatol. 26:120-128 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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PROSITE; PS50835; IG
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SMART; SM00406; IGV; 1
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GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
                                                                       DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLTESPP
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                                                                                                                                                                                                                                   Score 763; DB 6;
Pred. No. 1.8e-55;
1; Mismatches 15
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Pred. No. 1.8e-55;
1; Mismatches 15
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O02805; O77553;
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-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 3 C2-LIKE DOMAINS.
EMBL; AF001726; AAB60873.1; -.
EMBL; AF0577380; AABC0874.1; -.
EMBL; AF0577380; AABC25124.1; -.
EMBL; AF0577380; AABC25124.1; -.
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Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J.,
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0006955; P:immune response; IEA. InterPro; IPR000973; CD4 TCAg. InterPro; IPR007110; Ig-Tike. InterPro; IPR003596; Ig_v.
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MO1. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
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TISSUE=Peripheral blood;
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NCBI_TaxID=9534;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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CD4 (T-cell surface antigen
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Pfam; PF00047; ig; 2.

PRINTS; PR00692; CD4TCANTIGEN.

SMART; SM00406; IG; 3.

SMART; SM00406; IG; 1.

PROSITE; PS50835; IG LIKE; 1.

SEQUENCE 457 AA; 50878 MW; 7
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"Blockade of HIV-1 Infection of New World Monkey Cells
Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphocyte antigen CD4.
Callithrix jacchus (Common marmoset).
Cularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
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85.0%; Pred. No. 4.6e-55;
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MEDLINE=22174698; PubMed=12186836;
MEDLINE=22174698; PubMed=17.86836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 Infection of New World Monkey Ce.
Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445(2002).
J. Exp. Med. 196:431-445(2002).
EMBL; AF452617; AAN14533.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016955; P:immune response; IEA.
InterPro; IPR000599; Ig.
InterPro; IPR000599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-y.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00409; IG; 3.
SWART; SM00409; IG; 3.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 457 AA; 50899 MW; B
     01-NOV-1999
01-NOV-1999
01-OCT-2003
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Lymphocyte antigen CD4.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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O1-MAY-1997 (TrEMBLrel. 03, Last annotation up...
O1-OCT-2003 (TREMBLRel. 25, Last annotation up...
CD4 antigen precursor.
CD4 antigen precursor.
(Cat), Felis silvestria catus (Cat),
Felis silvestria catus (Cat),
Felis silvestria; Carnivora; Fissipedia; Felidae; Pelis.
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"Molecular cloning and characterization of
the white whale Delphinapterus leucas.";
Immunogenetics 49:376-383(1999).
IMMUNOGENETICS 49:376-383(1999).
IMMUNOGENETICS 49:376-383(1999).
IMMUNOGENETICS 49:378-1;
IMMUNOGENETICS 49:378-1;
IMMUNOGENETICS 1 IMMUNOTATION IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR0001710; Ig-Tike.
InterPro; IPR0001710; Ig-Tike.
InterPro; IPR0001596; Ig_v.
Pfam; PF00047; 1g; 3
PRINTS; PR00649; CD4TCANTIGEN.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 455 AA; 50499 MW; AA532FD44111
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Delphinapterus leucas (Beluga whale).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLVVMRVTKSPNSLTCEVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TKNQVSLTCLVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LTFGDENLSGELSWL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWTCTVSQAQQTLVFNKHILVLAFQEVSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILGRHGYFWHKGASNLHSRVESKINLWDQGSFPLVIKDLEVPDSGTYICEVEDKKIEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKLNNGKVTVGKARKDLKLRMS-KAL--
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                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NG-----KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL----
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Pred. No. 7.1e-42;
3; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356
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EMBL; AB000483; BAA1914...,

HSSP; P01730; 1WIQ.

A GO; GO:0016020; C:membrane; IEA.

R GO; GO:0006955; P:immune response; IE

JR InterPro; IPR000973; CD4 TCAg.

R InterPro; IPR0007110; Ig-Ike.

DR InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 3.

R Pfam; PF00047; ig; 3.
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Best Local Sim
Matches 121;
Proc. Natl. Acad. Sci. U.S.A. 84:7/
ENBL; M17080; AAA37402.1; JOINED.
ENBL; M17077; AAA37402.1; JOINED.
ENBL; M17077; AAA37402.1; JOINED.
ENBL; M17078; AAA37402.1; JOINED.
ENBL; M17079; AAA37402.1; JOINED.
ENBL; M17079; AAA37402.1; JOINED.
HSSP; P01730; IWBR.
                                                                                                                                                                                                                                                       Q61396;
Q61396;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
CHAIN
                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88041159; PubMed=2823269;
Gorman S.D., Tourvieille B., Parn
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                01-NOV-1996
01-OCT-2003
                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                   T-cell differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A cDNA encoding feline CD4 has a unique the V-like region."; Immunology 75:74-79(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyazawa T.;
Submitted (JAN-1997)
[2]
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MEDLINE=92165316; PubMed=1537604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                               Structure of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norimine J., Miyazawa
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                                                                                                                                                                                                                                                                                                                                           SKSGVHSLSLSQLELQESGTCTCTVSQSQKTLVFNTNIL
                                                                                                                                                                                                                                                                                                                                                                                                        QLLVFGLTANSD-------THLLQGQSLTLTLESPPGSSPSVQCRSPRGK
                                                                                                                                                                                                                                                                                                                                                                NIOGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                          ELLVFGLTAKVDPSGSGGSSSSSTSTSTSIYLIGGQSLTLTLESPSSSNPSVQWKGPGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KILGNQGSFL-TKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                        KILESQHSSLCLTGSSKLKTRFESKKILWDQGSFPLVIKSLQVADSGIYTCEVENKKREV
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' 27
474 AA;
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                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52243 MW;
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                                                                      U.S.A. 84:7644-7648(1987)
                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawaguchi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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Pred. No. 3.
                                                                                              encoding
                                                                                                            Parnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                           sequence update)
                                                                                        J.R.;
ng CD4 and an unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG
                                                                                                                                                                                                                               update)
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                                                                                               transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                  : 161
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Best Local Similarity
Matches 103; Conserv
                                                           SEQUENCE FROM N.A.

Maddon P.J., Molineaux S.M., Maddon D.

Alt F.W., Chess L., Axel R.;

Submitted (FEB-198) to the EMBL/GenE

EMBL; AF045882; AAC01764.1; -.

HSSP; P01730; IMBR.

MGD; MGI.88335; Cd4.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IE

InterPro; IPR000973; CD4 TCA9.

InterPro; IPR000973; GD4 TCA9.

InterPro; IPR000973; GJ-Ike.

InterPro; IPR0001973; Ig-Ike.

InterPro; IPR0001973; CD4 TCA9.

Pfam; PF00047; Ig; 2.

Pfam; PF00047; Ig; 2.

Pfam; PF00047; IG; IG_LIKE; 1.

NON TER PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88335; Cd4.
GO; GO:0015020; C:membrane; IEA.
GO; GO:0006955; P:immune response; II
InterPro; IPR000973; CD4_TCA9.
InterPro; IPR009710; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 457 AA; 51368 MW; 24ABI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998
01-JUN-1998
01-OCT-2003
      PROSITE;
NON TER
NON TER
SEQUENCE
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alt F.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maddon P.J., Molineaux S.M., Maddon D.E., Zimmern
Alt F.W., Chess L., Axel R.;
"Structure and expression of the human and mouse
Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surface glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRH-LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LODSGTWTCTVLQNQKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCRAISLRRLLLLLLQLSQLLAVTQEKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR
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433
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse).
      ΑΑ,
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Rodentia;
         48590
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06, Last seq
25, Last ann
(Fragment).
    MW;
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Last annotation updat
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Pred. No. 1.3e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                               Maddon D.E., Zimmerman K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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      AB19330750A8499A CRC64;
                                                                                                                                                                                                                              IEA.
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thi; Muridae; Murinae; Mus
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..3e-30;
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Best Local
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                                                                                                                                                                                                                                                           SIMILARITY).

SIMULARITY).

SUBGUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY)

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (B

-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERF

ONE V-LIKE AND 1 C2-LIKE DOMAIN.

EMBL; AF057386; AAC25130.1; -.

EMBL; AF057386; TCDY.

EMBL; AF057386; TCDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 077596; PRELIMINARY;
077596; PTEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                          "Nuclear gene trees and the phylogenetic relationships of mangabeys (primates: Papionini).";
MO1. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/1
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mandrillus sphinx (Mandrill) (Papio sphinx).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae;
NCBI_TaxID=9561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell surface glycoprotein
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                 [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment
                                                                                                                                                                                                                                             interPro;
                                                                                                                                                                                                                                                        GO:0016021; C:integral to membrane;
                         167
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92; Conserv
                                                                                                                 Similarity
                                                                YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-SFLTKG--PSKLNDRA
RTLSVPQLERQDSGTWTCTVSQDQK 85
                KTLSVSQLELQDSGTWTCTVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSKKGAWEKGSFPLIINKLKWEDSQTYICELENRKEEVELWVFKVTFSPGTSLLQGQSLT
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                                                YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLRVQDSDFWNCTVTLDQKK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQRKILGQHGKGVLIRGGSPSQF-DRF
                                                                                                                                                                                                                           IPRO07110; Ig-like.
bulin domain; T-cell; MHC; Transmembrane.
                                                                                                    Conservative
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86
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78
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Last annotation update)
CD4 (T-cell surface ant
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                                                                                                  Score 400; DE
Pred. No. 5.5e
6; Mismatches
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BY SIMIL
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Pred. No. 4.4e-28;
9; Mismatches 47
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                                                                                                                                                                               SIMILARITY.
                                                                                                                                                                                           V-TYPE DOMAIN.
C2-TYPE DOMAIN
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5.5e-26;
3;
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ULIN SUPERFAMILY.
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                                                                                                                                                     CRC64;
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                                                                                                                          Length 86;
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RESULT 077597

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ACC PRINT RAY
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Best Local S
Matches 76
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O1-NOV-1998 (TrEMBLrel. 08, Cr
O1-NOV-1998 (TrEMBLrel. 08, Lr
O1-OCT-2003 (TrEMBLrel. 25, L
          MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.; "Nuclear gene trees and the phylogenetic mangabeys (primates: Papionini)."; Mol. Biol. Evol. 15:892-900(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
GO; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-I- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mandrillus leucophaeus (Drill) (Papio leucophaeus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe Cercopithecinae; Mandrillus.
NCBI_TaxID=9568;
                                                                                                           Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
Cercopithecinae; Cercopithecus.
                                                                                                                                    Eukaryota;
                                                                                                                                                    Cercopithecus mitis
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DOMAIN
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                              (Fragment)
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P; P01730; 1CDY.
GO:0016021; C:integral to membrane;
cerPro; IPR007110; Ig-like.
cerPro; IPR007110; T-cell; MHC; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND I C2-LIKE DOWAIN.
L; AF057387; AAC25131.1; -.
FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
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                                                                                                  TaxID=36225;
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                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Last annotation update)
CD4 (T-cell surface antigen T4/LEU-3)
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                                                                                                                                                                                                               Created)
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Pred. No. 5.5e
6; Mismatches
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Last annotation updat
CD4 (T-cell surface a
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IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2BD97A9EE19582AB CRC64;
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                     85
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.5e-26;
                                   relationships
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                                    of.
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Best Local
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SEQUENCE
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DOMAIN
DOMAIN
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SEQUENCE
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Immunoglobulin domain; T-cell; MHC;
NON TER
1
DOMĀIN
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                                                                                                                                                                                                                             HSSP;
GO; GO
                                                                                                                                                                                                                                                   EMBL; AF057389; AAC25133.1; ~. HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                 mangabeys (primates: Papionini).";

Mol. Biol. Evol. 15:892-900(1998).

-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae;
NCBI_TaxID=9565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, T-cell surface glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMII-
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
ONE V-LIKE AND 1 C2-LIKE DOWAIN.
EMBL; AF057381; AAC25125.1; -.
                                                                                                                                                                                                                                                                                       -i- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theropithecus gelada (Gelada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nuclear gene trees and the phylogenetic relationships
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris E.E., Disotell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                             GO:0016021;
                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
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Similarity
                                                                                                                                                                                      lobulin domain;
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                                                                                                                                                                                                   IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 (TrEMBLrel. 08,
8 (TrEMBLrel. 08,
3 (TrEMBLrel. 25,
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16.4%;
88.2%;
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                                                                                                                                                                                T-cell; MHC; Transmembrane.
                                                              Ψ.
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Last annotation update)
CD4 (T-cell surface antigen T4/LEU-3)
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Pred.
Score 397;
Pred. No. 9
                                                              2BD97A98574EE9AB
                                                                                                     IG-LIKE V-TYPE DOMAIN IG-LIKE C2-TYPE DOMAII BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   baboon).
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No. 9.
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DB 6;
.8e-26;
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Best Local S
Matches 135
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS508290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96EY0;
Q96EY0;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC011857; AAH11857.1; -.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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108 135; Conservative
        270
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        HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-
                                                                                                            CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                             QVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDT
                                                                                                                                                                                                                 VSQLELQDSG-----
                                                                                                                                                                                                                                                                                                                        LTLTLESPPGSSPSVQCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTVGLFYWGQGTLVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNOFSLKLSSVTAADTAVYYCASOPWEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYIC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAG
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                                                                                                                                                                                                                                                                 LPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTD
                                                                                                                                                                                                                                                                                                                                                                         KYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNVP
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613 AA; 67273 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.4%; Score 395.5; DB 4; 22.2%; Pred. No. 1.9e-24; tive 83; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19,
19,
25,
                                                         -VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEA
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Last annotation update)
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RESULT 38
077598
ID 077598
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077595
ID 07759
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                                                                                                                                     맑
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
DISULFID
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O77595;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris E.E., Disotell T.R.; phylogenetic relationships of the "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini)."; mol. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercocebus galeritus chrysogaster.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016021; C:integral to membrane; InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN ONE V-LIKE AND 1 C2-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae;
NCBI_TaxID=75569;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin
NON TER 1
DOMĀIN <1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF057382; AAC25126.1;
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          077595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEP 525
                                                                                                                                                                                                                                         YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPRGKNIQGG
                                                                                                                                                                                                                                                                                    YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
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                                                                                                                                  RTLSVPQLERQDSGTWTCNVSQDQK
                                                                                                                                                                                     KTLSVSQLELQDSGTWTCTVLQNQK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AA;
                                                                                                                                                                                                                                                                                                                                                Conservative
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
49
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9419
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>86
79
78
                                                                                                                                                                                                                                                                                                                                                                                              16.4%;
                                                                                                                                                                                                                                                                                                                                                                         88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
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Last annotation update)
CD4 (T-cell surface antigen
                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                      Score 395; DB 6;
Pred. No. 1.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A9D97A9EE19582BE CRC64;
     PRT;
                                                                                                                                                                                                                                                                                                                                                Mismatches
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IEA

CONTAINS

Transmembrane

(POTENTIAL)

98

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-TEGEVSADE

580 443

Euteleostomi,

T4/LEU-3)

85

Length

Indels

<u>0</u>

Gaps

166 60

98

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QRWUK1
ID QRWUK1
ID QR
AC QR
DT 01
DT 01
DT 01
DT 01
DT 01
RR Hy
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OX NC
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057388; AAC25132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WUK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                Strausberg R.;
Submitred (DEC-2001) to the
EMBL; BC020240; AAH20240.1;
PIR; PL0120; PL0120.
PIR; S15590; S15590.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMĀIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).", Mol. Biol. Evol. 15:892-900(1998).

-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio sp. (
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    077598;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998
01-OCT-2003
                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Tonsil;
                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell surface
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                            nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                b; ARUSIAN, ICDY.
PO1730; ICDY.
GO:0016021; C:integral to membrane; IEA.
GO:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTLSVSQLELQDSGTWTCTVLQNQK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSSPSVQCRSPRGKNIQGG
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     IPR007110;
IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Baboon) .
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Gremburel.
Gremburel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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8496
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IremBLrel. 08,
IremBLrel. 25,
e glycoprotein
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>86
79
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86
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                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
Ig-like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.2%;
87.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 250,
                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
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Last sequence update)
Last annotation update)
CD4 (T-cell surface ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A9D97A98574EE9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Eutele
Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                       Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392; DB 6;
No. 2.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613
                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTIAL)
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A Straubberg R.;

A Straubberg R.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databa

R EMBL; BC009851; AAH09851.1; -.

R PIR; S15590; S15590.

R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity; IEJ

JR GO; GO:0003700; F:regulation of transcription, DNA-c

InterPro; IPR0000005; HTHAraC.

InterPro; IPR0007110; Ig-like.
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Piam; PF00047; ig; 5.
SMART; SM00406; IGv; I.
SMORT; P850835; IG_LIKE; 5
PROSITE; P850835; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96GA6;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                    TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96GA6
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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23.9%;
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Pred. No. 6.2e-
77; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
annotation update)
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pfam; pF00047; Ig; 5.

smART; sm00406; IGv; 1.

pROSITE; pS00041; HTH ARAC_FAMILY_1; 1

pROSITE; pS50835; IG_LIKE; 5.

PROSITE; PS000290; IG_MHC; 3.

Hypothetical protein.

SEQUENCE 614 AA; 67921 MW; 55EF536)
                                                                                                                                                      Q96AA6 PRELIMINARY; PRT; 618 AA.
Q96AA6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           Strausberg R.;
Submitted (NOV-2001) to the
EMBL; BC017356; AAH17356.1;
PIR; S15590; S15590.
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=9606;
  InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                     TISSUE=Lymph;
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                             SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLWAT
                                                                                                                                                                                                                                                                                                                                                                              GLWTT
                                                                                                                                                                                                                                                                                                                                                                                                        RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELODSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESPPGSSPSVQCR------SPR------GKNIQGGKTLSVSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVLRGGKYAATSQVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----FP
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                                                                                                                                                                                                                                                                                                                                                                              452
                                                                                                                                                                                                                                                                                                                                                   590
Ig-like.
Ig_MHC.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 389.5; DB 4; 23.9%; Pred. No. 6.2e-24; tive 77; Mismatches 167;
                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                          databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                     447
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NCBI_TaxID=75568;

Lophocebus albigena albigena. Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercopithecinae; Lophocebus.

Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;

SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
MOI. Biol. Evol. 15:892-900(1998).
-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY SIMILARITY).
-!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).

O77601;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface a

tion update) surface ant

antigen

T4/LEU-3)

077601

PRELIMINARY;

PRT;

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RESULT 42
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig;
                                                          448
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                                                                                                                                      333
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                                                                                                                                                                                                                                     311
                                       590
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                                                                                                                 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                                                                                                                                                                                                   EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                   LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT
                                                                                                                                                                                                                                                                                                                                                                          TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                      NLWAT
                                                         GLWTT 452
                                                                            RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS----TEGEVSADEEGFE
                                                                                                                                                                                            -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
                                                                                                                                                                                                                 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                       ELQDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                          AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
                                                                                                                                                                                                                                                                                              LESPPGSSPSVQCR------SPR-----GKNIQGGKTLSVSQL
                                                                                                                                                                                                                                                                                                                SVLRGGKYAATSQVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                                       SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    67758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     16.1%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   `3`5.
                                                                                                                                                                                                                                                                                                                                                                                             77;
                                                                                                                                                                                                                                                                                                                                                                                             Score 389.5; DB 4
Pred. No. 6.2e-24;
7; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                    96DBD4C7C696E0A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                              167;
                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                447
                                                                                                                                      387
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                                                                                                                                                                                            A Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC002963; AAH02963.1; -.

R HSSP; P01825; 7FAB.
R InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Ffam; PF00047; ig; 5.
R Pfam; PF00047; ig; 5.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS050835; IGV; 1.
R PROSITE; PS050835; IG LIKE; 5.
R PROSITE; PS0290; IG_MHC; 3.

M Hypothetical protein.

M Hypothetical protein.
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Best Local S
Matches 74
                                                                                                                                                 Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BU10;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
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DOMAIN
DISULFID
NON_TER
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-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057391; AAC25135.1; -.
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IFR007110; Ig-like.
Inmunoglobulin domain; T-cell; MHC; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lympn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
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                          150
  258
                                                                                                  167
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                        SPSVQCR----
                                                                        LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
                                                                                                  SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
                                                                                                                       TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTLSVPQLERQDSGTWTCTVSQDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTLSVSQLELQDSGTWTCTVLQNQK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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>86
78
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                                                                                                                                               15.9%; Score 385; DB 4; 24.9%; Pred. No. 1.4e-23; cive 73; Mismatches 164
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Last annotation updat
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Pred. No. 5.
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IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2BD97A88464FE9AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                       ----SPR-----GKNIQGGKTLSVSQLELQDSG- 180
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.6e-25;
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                                                                                                                                                                       Length 597;
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                                                                                                                                                 Indels
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Q9BQBB
ID Q9BQB
AC Q9BQB
AC Q9BQB
DT 01-TU
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DT 01-GC
DE Hypot
OS Homo
OC Eukax
OC Mamma
OX NCBI
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RN [1]
RN [1]
RN SEQUE
RC TISSUE
RA Strau
RL Submi
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DR HSSP;
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Best Local Sim
Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9BOB8
O9BOBB;
O1-JUN-2001 (TrEMBLrel. 17, Cr
f 01-JUN-2001 (TrEMBLrel. 17, Lr
cory-2003 (TrEMBLrel. 25, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
SMOSTIE; PS00835; IG LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (ARR-2001) to the EMEMBL; BC006180; AAH06180.1; -. EMBL; BC0061872; AAH01872.1; -. HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Muscle, and Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                      221
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                                                                                                                                                                                                                                                                                    94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
                                                                                                                                                                                                                                                                                                                                                                      36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                    GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                               TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR--
                                                                                                                                                   SVFVPPRDGFFGNPRKSKLICOATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                   SPSVQCR---
                                                                                                                                                                                                                                         SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VFAIPPS-FASIFLIKSTKLICLVIDLTTYD-SVIISWTRONGEAVKTHINISESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQLINERSATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%;
-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                          ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 385; DB 4;
Pred. No. 1.4e-23;
73; Mismatches 164
                                                                                                                                                                                              ----SPR-----GKNIQGGKTLSVSQLELQDSG- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2DAFAD50A6375851 CRC64;
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AC Q96BB
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DT 01-OC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
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01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96ВВ9;
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TISSUE=B-cell;
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RDELT-KNQVSLTCLVKGFYFSDIAVEWESNGQP--ENNYKTTFPVLD--SDGSFFLYSK 394
                                                                             PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                          YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS 339
                                                                                                                                                                                                                                  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                          SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSVQCR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
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                                                                                                                                                                                                                                                                                     TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR------
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597 AA; 6
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VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 385; DB 4; 24.9%; Pred. No. 1.4e-23; tive 73; Mismatches 164
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19,
25,
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                                                                                                                                                                                                                                                                                                                                     --TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local S
Matches 73
                                                         01-OCT-2003 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
Hypothetical protein.
Mus musculus (Mouse).
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NON TER
SEQUENCE
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077600;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TEMBLrel. 08, 01-NOV-1998 (TEMBLrel. 08, 01-OCT-2003 (TEMBLrel. 25, T-cell surface glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                              Q7TMT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain,
NON TER 1 1
DOMĀIN <1 19
DOMAIN 20 >86
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057390; AAC25134.1; -.
HSSP; P01730; 1CDY.
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Mammalia; Eutheria; Primates;
    NCBI_TaxID=10090;
                                                                                                                                                                          Q7TMT6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016021; C:integral to membrane; InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                KTLSVSQLELQDSGTWTCTVLQNQK
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                        Rodentia;
                                            Chordata;
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n; Glycoprotein; T-cell; MHC;
                                                                                                       25,
                                                                                                       Created)
Last seq
Last ann
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Pred. No. 1.5e
7; Mismatches
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Last annotation update)
CD4 (T-cell surface antigen
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IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL) .
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A9D97A88464FE9BE CRC64;
                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Simi
Matches 139;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S. T. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC053409; AAH53409.1; -. Hypothetical protein. SEQUENCE 614 AA; 67746 NW; 839BAF3B8D124F89 CRC64;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
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    479
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                          DELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLYSKL
                                                                                                      RVVSVLTVLHQDWLNGKEYKCKVSNKALFAPIEKTISKAKGQPRE-----PQVYTLFPSR
                                                                                                                                                                                                                                                                                                                                    VAEMNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPV
                                                                                                                                                                                                                                                                                                                                                                                                                       VIQGIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNKDLH---VPIPA
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EQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSIL
                                                                                                                                                                                                                                                   TIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----WTCTVLQNQKKVEFKIDIVPCPA
                                                                                  SAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLPPAR
                                                                                                                                                                   FTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTF
                                                                                                                                                                                                          FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
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Pred. No. 3
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RESULT 48
Q8WUX4
ID Q8WUX4
ID Q8WUX
AC Q8WUX
DT 01-W2
DT 01-W2
DT 01-O0
OC EUkaa
OC EUkaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
PROSITE; PS00290; IG MHC; 3
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Q8WUX4;
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Hypothetical protein.
SEQUENCE 588 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2002
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542
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                                                                                                                                                                                    281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                      REQUNIRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRVFAHSI 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                 SPSVQCR-----SPR-----GKNIQGGKTLSVSQLELQDSG- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG--
LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS
                               LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                       RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
                                                                                                                                                PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                                                                                    YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                                                                                                                                                                                                                            GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                   TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR------
                                                                                                                                                                                                                                                                                                                                                                            SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVTEEEWNSGETYTCVVSHEALPHLVTERTVDKS-----TEGEVNAEEEGFENLWTT
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                                                                                                                                                                                                                       VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64438 MW; FC60DBAD82B39FD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
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                                                                                                                                                                                                                                                                                                                                     ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 380; DB 4; I
Pred. No. 3.6e-23;
3; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                     429
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                                                                                                                                                481
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RESULT 49 Q8VCX7

Q8VCX7

PRELIMINARY;

PRT;

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RESULT 50
Q86TT1
ID Q86TT
AC Q86TT
DT 01-JU
DT 01-OC
DE Human
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC018315; AAH18315.1; -.
MGD; MGI:96448; Igh-6.
InterPro; IPR007710; Ig-1ike.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
SMORTE; PS00835; IG_IIKE; 5.
PROSITE; PS00835; IG_MC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VCX7;
01-MAR-2002
01-MAR-2002
01-OCT-2003
      Q86TT1 PRELIMINARY; PRT; 375 AA.
Q86TT1;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Human full-length cDNA clone CSODD006YL02 of neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (DEC-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical IGH-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                               535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
  (Human
                                                                                                                                              SILTYTEEEWNSGETYTCVVGHEALPHLVTERTVDKS----TEGEVNAEEEGFENLWTT
                                                                                                                                                                     SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                  PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                      GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                   STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                                                                                         --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                            YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST-----DIL--
                                                                                                                                                                                                                                                                                                                                                                                 ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPP----GSSP---SVQCR----SPR-----GKNIQGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSQVLLSPKSILEGSDEYLVCKIH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT------LRTGGKYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                  PAREQUILLESATVICLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 373.5; DB 11;
Pred. No. 1.4e-22;
7; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YG-GKNRDLHVPIPAVAEMNPNVNVF
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             С
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             Homo
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Best Local :
                                                                                                                   Q13969;
Q13969;
Q1-NOV-1996
Q1-JAN-1999
Q1-OCT-2003
SEQUENCE FROM N.A.
Zverev V.V., Blinov V.M.,
"Splice-mediated insertion
                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 3.
SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BX151420; CAD61894.1; -. GO; GO:0046821; C:extrachromosomal InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_c1.
                                                                                                         CD4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li W.B., Gruber C., Jessee C
"Full-length cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Neuroblastoma;
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                                                                                                                                                                                                                                                       389
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                                                                                                                                                                                                                                                                                                                            NISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                               VSQLELQDSG----TWTCTVLQ----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                               YFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                                                                                                                                                                                                                                       FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                          YTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGS
                                                                                                                                                                                                                                                                                                                                               KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV
                                                                                                                                                                                                                                                                                                                                                                          CGPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT
                                                                                                                                                                                                                                                                                                                                                                                                 GGPS-----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                         QVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLTLESPPGSSPSVQCR------SPR-------GKNIQGGKTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTD
                                                                                                                                                                                                                                                                              YLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jruber C., Jessee J., Polayes D.;
Jth cDNA libraries and normalization
(JAN-2003) to the EMBL/GenBank/DDBJ
(JAN-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAN-2003)
                                                                                                        (TrEMBLrel. () (TrEMBLrel. () (TrEMBLrel. ) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AA;
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                                                                                                                                                                     PRELIMINARY;
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 insertion
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                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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 Nedospasov S.F
n of antisence
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Last
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                                                                                                                                             Created)
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Pred. No. 2.7e-22;
                                                           Craniata; V
Catarrhini;
                                                                                                                                                                     PRT;
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                                                                                                                      sequence update) annotation updat
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            S.A.;
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 and
                                                                      Vertebrata;
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                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
 sence
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                                                                         Euteleostomi;
                                                                                                                                                                                                                                                       431
                                                              Homo
                                                                                                                                                                                                                               356
 repeats
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  human
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RESULT
Q7TOR1
       PRESENTATION OF THE PRESEN
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Best Local S
Matches 70
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Q7T0R1;
01-OCT-2003
                  MEDLINE-23388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Sanchez A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
NON_TER
SEQUENCE
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Vopr. Virusol. 40:100-102(1995)
EMBL; X87579; CAA60883.1; -.
EMBL; S79267; AAB35273.1; -.
PIR; 160082; 160082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4 gene:
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95407135; PubMed=7676667;
Zverev V.V., Sidorov A.V., Nedospasov S.A.,
Udalova I.A., Andzhaparizde O.G., Blinov V.!
"[Nucleotide sequence of two exons of the h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S.L., St
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917; Klein S.L., Strausberg R.L., Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiative."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (enopodinae; Xenopus.
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P; P01730; ICDY.
GO:0004872; F:receptor activity;
cerPro; IPR007110; Ig-like.
pss0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TaxID=8355;
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Helton E., Ketteman M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225:384-391 (2002)
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AA;
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7844 MW;
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98.6%;
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Pred. No. 1.7e-
0; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
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Best Local S
Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 587 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (AUG-2003) to the
EMBL; BC056078; AAH56078.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissuE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
546
                         405
                                                   486
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                                                                  LVKGFYPSDIAVEW--ESNGQPENNYKTTP-----PVLDSDGSFFLYSKLTVDKSRWQQ
                                                                                                         CADEWNNDK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC
                                                                                                                      FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD
                                                                                                                                                                                                                                                                                                                     AVWD--NIEQFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI
GDSFSCVVGHESLPLQLTQRSIDKSSGKPTNVNVSLVLSDTC
                         GNVFSCSVMHEALHNHYTQKSLSLSPG-----LQLDETC
                                                  LVKGFSPSEIFVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDA
                                                                                                                                                           FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV
                                                                                                                                                                                      MISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV
                                                                                                                                                                                                                DTLYSCVV
                                                                                                                                                                                                                                         SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL
                                                                                                                                                                                                                                                                   VCLATNETPTHI -----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL
                                                                                                                                                                                                                                                                                                                                                 SLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ-------
                                                                                                                                                                                                                                                                                                                                                                          GESMDPVTIGCLAKDFLPETISFTWGDKNNASYSTGLKSYKPVMQSSGTYSASSQVNVAS
                                                                                                                                                                                                                                                                                                                                                                                                     GKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSF----LTKGPSKLNDRADSRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64933 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                -EHAESGSLQEKNMSKSLMCDTPITPTSIQVITIPPS-LESI
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 345.5;
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Butterfield
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587
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RESULT 53
Q7Z379
Q7Z379 PRELIMINARY; PRT; 478 AA.
Q7Z379;
Q1-QCT-2003 (TrEMBLrel. 25, Created)
Q1-QCT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment).
DKFZP686K04218.
        TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/Geni
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      NCBI_TaxID=9606;
                                                                                                                            Homo sapiens (Human)
                                                              EQUENCE FROM
                                                              N.A.
                                                                                                   Chordata;
Primates;
          EMBL/GenBank/DDBJ
                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae
                                   Weil
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                                                                                                   Hominidae;
                                    Amid
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                                                                                                                 Euteleostomi;
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Osanger

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Q7237

ID Q7237

AC Q7237

O1-OC

DT 01-OC

DT 01-OC

DE Hypot

GN DKFER

OC Eukar

OC Eukar

OC Mammas

OC Mammas

OC MAMMas

OC TISSI

RN [1]

RP SEQUE

RA Bloec

RA FODO

RL Submii

KW Hypot

KW Hypot

KW Hypot

FT NON SEQUE
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Best Loc
Matches
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Best Local S
Matches 135
                          Query Match
                                                                                                                                                                                                                                                                                                 Q7Z374;
Q7Z374;
01-OCT-2003
01-OCT-2003
                                                                                        TISSUE-Human rectum tumor; Bloecker H., Boecher M., Mewes H.W., Weil B., Fobo G., Han M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; BX538077; CAD98001.1; ...
                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein DKFZp686C02218 (Fragment)
DKFZP686C02218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
NON TER 1
SEQUENCE 478 AA; 5
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                        SEQUENCE
                                                                     Hypothetical protein.
                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                     EQUENCE FROM N.A.
Local Similarity
mes 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANITKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGESPKDVLVRWLQGSQELPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKTISKAKGQPREPQVYTLPPSRDELTKNQ-V5LTCLVKGFYPSDIAVEWESNGQ--PEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E---SGONVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLEL----QDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGTAFDIWGQGTVVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIKNLKIEDSDTYIC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKK--SIQFHWKNSNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYKTTPPVLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTVPCPVPPPPPC-----C----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGRGLEWMGYIYYSGSTYYNPSLESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVG
                                                                                                                                                                                                                                                                                                                                                                                                                  KPTHVNVSVVMAEVDGTC
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                                                        492
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 Conservative
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                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                      1
53776 MW;
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27.1%;
           13.4%; Score 322.5; DB 4
26.3%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
68;
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Pred. No. 1.
                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                        1E7A15760F0CA74B
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Mismatches 211;
                                                                                                                                                                                                                                                                                                                                            492
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                         DB 4;
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                                                                                                              databases
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                         Length
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Indels
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                                                                                                                                        Osanger
                            492;
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99;
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Gaps
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23;
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                                                    Matches
                                                                 Query Match
Best Local
                                                                                                                         PIR; F33932; F33932.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS508290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                               Q99LA6;
Q99LA6;
01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                               Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC003495; AAH03495.1; -
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                     Hypothetical protein. SEQUENCE 484 AA; 5
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431
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            VLQLALLPAATQGNKV------VLGKKGDTVELTCTASQKKSIQF--HWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPYGWFDPWGQGTLVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIKILGNQGSFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYIC--EVE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGGSVSNRNYYWGWIRQP
VWTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKYLTWASROEPSOGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTOKTIDRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWTHGETFTCTAAHPELKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DI-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SE---SGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLEL----QDSGTWTCTVLQNQKKVEFKI
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                                                                                                                                                                                                                                                                                                                                                                             1 (TrEMBLrel. 17,
1 (TrEMBLrel. 17,
3 (TrEMBLrel. 25,
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LQLDETC
                                                                                                      52567 MW;
                                                                                                                                                                                                                                                                                                                              Rodentia;
                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                              13.1%;
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                                                  67;
                                                   Score 315.5; D
Pred. No. 7.1e-
67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491
                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                      8EAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  484
                                                   7.1e-18;
hes 200;
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                                                                             DB 11;
                                                    Indels
                                                                           Length
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                                                                              484;
                                                   91;
                                                  Gaps
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Q9 CAA
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Best Local S
Matches 132
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Q99KA4;
Q1-JUN-2001 (TEMBLrel. 17, Cre.
Q1-JUN-2001 (TEMBLrel. 17, Las.
Q1-OCT-2003 (TEMBLrel. 25, Las.
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C1
Mammalia; Eutheria; Rodentia; S0, NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 487 AA; 52554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786; AAH04786.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_v.
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E-SGTLTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVRAPNPKEVLVRWLHGN
                            ----KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC
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QTPEKRLEWVATISDGGSY-TYYPDNVKGRFTISRDN-AKNNLYLQMSHLKSEDTAMYYC
                                                                                                       MNFGLSLIFLVLVLKGVQCEVQLVESGGGLV---KPGGSLKLSCAASGFTFSSYAMSWVR
                                                                                                                                                                 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW--
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                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                 13.0%; Score 314.5; DB 11; Length 487, 26.2%; Pred. No. 8.6e-18; Ative 76; Mismatches 188; Indels 107
                                                                                                                                                                                                                                                                                                                                  52554 MW; 7DC8E96DB333077B CRC64;
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Last annotation update)
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Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 118
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC01832; AAH18322.1; -.
R MGD; MG1:96486; Igh-VJ558.
R InterPro; IPR0070110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_V.
R InterPro; IPR003596; Ig_V.
RR Pfam; PF00047; 19; 4.
R Pfam; PF00040; IG; 1.
R SMART; SM00406; IGV; 1.
RR PROSITE; PS00290; IG_MHC; 2.
RR PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
IGH-VJ558 OR A1993585.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia, Eutheria; Rodentia;
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Q8VCX4;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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                                                    KATLTADKSSTTVYMDLSRLTSEDSAVYFCARHEDR------GNYDGSLAWFVYW 134
                                                                                                  RRSLWDQGNFPLI---IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL----LQ
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                                                                                                                                                            LVKPGASVKLSCKASGYTFSDYFIHWIKQRSGQGLEWIGWFNPGS----GSIKFNEKFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTLPAVECPEGESVK
                                                                                                                                                                                                                                                            13.0%;
llarity 24.9%;
Conservative 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                     53208 MW;
                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                            Score 313.5; DB 11; Length Pred. No. 1.1e-17; O; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                        CC85B1194DAFEF2C CRC64;
-QCRS---
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                                                                                                                                                                                                                                                               Indels 105;
  --PRG-KNI---QGGKTLSV 171
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                                                                                                                                                                                                                                                               Gaps
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Q9NPP6
ID Q9NPP
ID Q9NPP
ID Q9NPP
ID 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT 100-OC
DT Immun
OS HOMO
OC EUKAX
OC NCEN
RN [1]
RN [1]
RN SEQUE
RA Pluvi
RL Submi
RL Submi
RL Submi
RL Submi
RL Submi
RI [2]
RP SEQUE
RA Lehra
RT Submi
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DR SMART
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                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                Matches 116;
                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Auffray C., Ansorge W., Ballabio Lehrach H., Poustka A., Lundeberg "The Buropean IMAGE consortium fc human gene transcripts."; Submitted (UTL-2000) to the EMBL; AL38978; CAB97534.1; -. HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
Pluvinet R., Estivill X., Es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Immunoglobulin heavy chain variant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NPP6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NPP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
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                                                      79
                                                                                                                            19
                                                                                                                                                             78
                                                                                                                                                                                                                  Similarity
QGGKTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCP 217
                                                                                      ----LVFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNI 163
                                                                                                                          DYADSVKGRFTVSRDTAKNSLSLQMSSLRVEDTAVYYCARTYYGMDVWGQGTTVTVSSAS
                                                                                                                                                           DRADSRRSLWD-----QGNFPLIIKNLKIEDSDTYIC-----EVEDQKEEVQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ----PENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH-----TCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAK
                                                                                                                                                                                                                                                                      416 AA;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                      44786 MW;
                                                                                                                                                                                                                12.9%;
27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lundeberg i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballabio A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escarceller M., Sumoy L.;
he EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          ; Score 312; DB 4; Length 41; Pred. No. 1.1e-17; 61; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDG
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                                                                                                                                                                                                                                                                      8C41708BB8AB4687 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular analysis
                                                                                                                                                                                                                               Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibson
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Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 481 AA; 52105 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91WT1;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chemammalia; Eutheria; Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL, BC013490; AAH13490.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91WT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 24.7
120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
PB-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLDETC
                                                                            PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD
                                                                                                                                                                           VTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSN
                                                                                                                                                                                                                           I---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH---
                                                                                                                                                                                                                                                                         -TRGGGWAFDYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMN
                                                                                                                                                                                                                                                                                                                       GLTANSDTHLLQGQSLTLTLESPPGSSPSV-----
                                                                                                                                                                                                                                                                                                                                                                             IYPGDGNTKYNEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFC---
                                                                                                                                                                                                                                                                                                                                                                                                                        SFLTKGPSKLNDRADSRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSGPE-----LVKPGASVKISCKASGYTFTSYYIHW-----VKQRPGQGLVWIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPSEELALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPPC----C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HPRLSLHRPALED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                                                                                                          ----TCPELLGGPSVFLFPPKPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19,
19,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 311; DB 11;
Pred. No. 1.7e-17;
7; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187;
                                                                                                                          ----DTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                            -QCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 112;
                                                                                                                                                                                                                                                                                                                               PRG-KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415
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                                                                                                                             255
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                                                                                                  Query Match
Best Local (
                                                                                        Matches
                                                                                                                                InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGcl; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 482 AA; 52121 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8K172
Q8K172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893585.
                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL; BC028249; AAH28249.1; PIR; F33932; F33932. PIR; PH1105; PH1105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                          PH1125;
PH1126;
PH1128;
PH1131;
PH1134;
PH1139;
PH1139;
                                                                                                                                                                                                                                                                                     PH1149;
PH1150;
                                                                                                                                                                                                                                                                                                                                                                                                               PH1108;
PH1114;
                                                                                                                                                                                                                                                     PH1153; PH1153
                                                                                                                                                                                                                                                                                                                                                                                          PH1119;
                                                                                                                                                                                                                                                                                                                                                                                                      PH1118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
 88
                     85
                                            30
                                                                30
                                                                                                   Similarity
TLTVDKPSSTAYMQLSSLTSEDSAVYYCTRE------GDYDAMDYWGQGTSV
                     SLW----DOGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL
                                         LVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDP--NSGGTKYNEKFKSKA
                                                                LGKKGDTVELTCTAS---QKKSIQFHW---KNSNQIKILGNQGSFLTKGPSKLNDRADSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDRLSG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP
                                                                                        Conservative
                                                                                                                                                                                                                                                             PH11108
PH11114
PH11119
PH11125
PH1126
PH1128
PH1128
PH1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431
                                                                                                  12.9%;
                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases.
                                                                                                 Score 311; DB 11;
Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi;
                                                                                                                                    A06FF083E771D084 CRC64;
                                                                                      Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae;
                                                                                                            Length 482;
                                                                                        Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae; Mus
                                                                                        Gaps
133
                    141
                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396
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RESULT 61
Q91X92
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                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF000477; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 482 AA; 51865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91X92; PRELIMINARY;
Q91X92;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011181; AAH11181.1; -.
PIR; F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Colon;
                                                                                                                                                                                      123;
              158
                                      122
                                                               118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                        63
                                                                                                              61
                                                                                                                                                       10 LLLVLQLALLPAATQGNKVVLGKKG------DTVELTCTAS--QKKSIQFHWKNSNQIK
                                                                                                                                      4
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMDYW-
                                                                                     GLEWLGVIWTGGVTNYNSALKSRLSISKDNSKSQVFLKMNSLQTNDTARYYC-ARDSNYE
                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKEE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQXTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRG-KNI---
                                                              VOLLVFGLTANSDTHLLOGOSLTLTLESPPGSSPSV-----
                                                                                                                                     LALLICIVTFPSCAL-SQVQLKESGPDLVAPSQSLSITCTVSGFALTSYAISWVRQPPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLEPPKPK------DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH------TCPELLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGICSPPTT
                                                                                                                                                                                       Conservative
-QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD
                                                                                                                                                                                                                                      51865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                                                                                                   12.7%; Score 307; DB 11; 25.0%; Pred. No. 3.6e-17;
                                                                                                                                                                                       69;
                                      GOGTSVTVSSEPAREPTIYPLTFPOALSSDPVIIGCLIHDYF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                       Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on update)
                                                                                                                                                                                                             Length
                                                                                                                                                                                       Indels 102;
                                                               -0CRS---
                                                                                                                                                                                                                482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431
                                                                                                                                                                                       Gaps
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RESULT 63
Q91Z07
ID Q91Z0
AC Q91Z0
DT 01-DE
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ID Q2902
AC Q2902
DT 01-NC
DT 01-NC
DT 01-NC
DT 01-S
CD4,
OS Sus s
CC EUKar
OC Mamma
OX NCBI
RN (1)
RN (1)
RN SEQUE
RC STRAII
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RX 
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Best Local S
Matches 59
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Q29027;
Q19027;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-CTT-2003 (TrEMBLrel. 25, L
CD4, allele 1 (Fragment).
Sus scrofa (Pig).
  Q91Z07
Q91Z07;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
NON_TER
NON_TER
SEQUENCE
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gustafsson K., Germana S., Sundt T. "Extensive allelic polymorphion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=#1183; TISSUE=Blood;
MEDLINE=93329116; PubMed=8335933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420
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                                                                                                                                                                                     KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG
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                                                                                                                                                                                                                                                                                           KAGDLAELPCHSSQKKNLPFNWKNSNQTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAV
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     (TrEMBLrel. 19,
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
9 AA;
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11170 MW;
                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 305.5; 60.2%; Pred. No. 5.56 tive 16; Mismatches
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Last sequence update)
Last annotation update)
     Created)
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М.
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99;
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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  RESULT
Q8K0F2
Q8K0F2
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AC QR
DT 01
DT 
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                     Q8K0F2
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Matches 129;
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EMBL; BC010324; AAH10324.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-MHC.
InterPro; IPR003106; Ig_v.
InterPro; IPR00347; ig; 4.
Pfam; PF00047; ig; 4.
SMART; SM00406; IG-WHC; 2.
PROSITE; PS00290; IG-MHC; 2.
Hypothetical protein.
SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
OBKOF2;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                           CMVGHEAL PMNFTQKTIDRLSG
                                                                                                                                                                                                                 CSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                         KGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFS
                                                                                                                                                                                                                                                                                                                               ERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCLV
                                                                                                                                                                                                                                                                                                                                                                                                           GSDASLTCTLNGLRNPEGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VRPEIPIYYYSGSYFDS----WGQGTTITVSSESARNPTIYPLTLPRALSSDPVIIG
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                                                                             PRELIMINARY;
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25,
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; Pred. No. 5.4e-17;
79; Mismatches 188;
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Last annotation updat
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Matches 121;
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Submitted (JUN-2002) to the EMBI
Submitted (JUN-2002) to the EMBI
EMBL; BC031703; AAH31703.1; -.
InterPro; IPR007110; Ig-1ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_IKE; 4.
PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 488 AA; 53127 MW; (
Q90544 PRELIMINARY; PRT; 684 AA.
Q90544;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 21, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Novel antigen receptor precursor.
Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii, Galeemorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Colon;
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Pred. No. 6
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RESULT 66
Q91XE1
       DAFFEE 2000
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Best Local S
Matches 107
                                                               Q91XE1 PRELIMINARY;
Q91XE1;
01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-OCT-2003 (TrEMBLrel. 25, L
Hypothetical protein (Fragmen
Hypothetical protein (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNĀL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 6.
SMART; SM00407; IGc1; 4.
PROSITE; PS50835; IG_LIKE; 6.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A new antigen receptor gene family that undergoes extensive somatic diversification in sharks."; Nature 374 168-173 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004872; F:receptor activity;
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18701; AAB48195.1; -. PIR; S60266; S60266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenberg A.S., Avila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95183140;
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TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flajnik M.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
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                                                                                                                                                                                                                                                                                                 VVLSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKAK-GQPREPQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGO-PENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VELTCTASQKKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNFPL
                                                                                                                                                                                                                                                                                                                                                                                        QVDSEKGSGSSFVTDRLRLTAAEWNSDTTYSCLVGHPSLNRDLIRSTNKSNGKPSSVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ
                                                                                                                                                                                                                                                                                                                                            LOLDET
                                                                                                                                                                                                                                                                                                                                                                                                                                   TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WQVNGVERKKGVETQNPEWSGSKSTIVSKLKVMASEWDSGTEYVCLVEDSELPTPVKASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRSPRGKNIQGGKTLSVSQLELQDSGTWTCT------VLQNQKKVEFKIDIVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----CRQTDI-----SVSLLKP-PFEEIWTQQTATIVCEIV---YSDLENIKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LINLTAVEWKSGAKYTCTASHPPSQSTVKRVIRNQ
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75224 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
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Pred. No. 1.7e
66; Mismatches
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                        Created)
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NOVEL ANTIGEN RECEPTOR
, 2FF9D2071CDA6DFD CRC
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                            Euteleostomi;
    Murinae;
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RESULT 67
Q96K6
ID Q96K6
AC Q96K6
AC Q96K6
AC HOPT 01-DE
DT 01-OC
DT HYPOT
OC EUKaz
OC Mamma
OC NCBI
RP SEQUE
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Best Local S
Matches 121
                                                               Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003096; Ig-Y.
Pfam; PF000479; 19; 4.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG-MHC; 2.
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
NON TER 1
SEQUENCE 480 AA; 5
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Similarity 24.2%; Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                             MVGHEALPMNFTQKTIDRLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAE
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Best Local S
Matches 123
                                                                       Q91WT3;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                       Hypothetical IGH-VJ558 OR
                                                                                                                                                                             Q91WT3
  musculus
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50830590; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Mammary gland;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.
Watanabe S., Kimura K., Murakawi K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027379; BAB55072.1; -.
EMBL; AK027379; BAB55072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 494 AA; 5
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                                                                                                                                                                                                          S-RDNAKNSLYLQMN-----SLRVDDTAVYYCARDSCNGAI---CYGFSP------WG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSLTLTLESPPGSSPSV----QCRSPRGKN-----IQG---GKTLSVSQLE
EVDGTC
                                                 OLDETC
                                                                                                       QGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMA
                                                                                                                                                      DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG---
                                                                                                                                                                                                                                                                                                                                                                HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKÇKVSNKALPAPIEKTISKAKGQPR
                                                                                                                                                                                                                                                                                                                                                                                                                          PSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYYRDSVKGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
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     493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TWTCTVLQNQKKVEFKI-----DI-VPCPAPEPKSCDK
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(Tremblrel. (Tremblrel. (Tremblrel. (Tremblrel. l protein. R AI893585.

19, 19, 25,

> PRT; Created)

Last sequence update)
Last annotation updat

PRELIMINARY;

481 AA

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Query Match
Best Local S
Matches 121
                                                                Q8VEAO PRELIMINARY;
Q8VEAO;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-QCT-2003 (TrEMBLrel. 2
Hypothetical protein.
IGH-VJ558 OR A1893585.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 2.
    Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC013488; AAH13488.1; -. MGI:96486; Igh-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWL
                                                                                                                                                                                                                                                                                                                                                                             HEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                             PKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSDIAVEWESNGQ----PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGASFKCTVTHPESDT-LTGTTAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPKSCDKTH-----TCPELLGGPSVFLFPPKPK-----DTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PRG-KNI----QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWIGAIDPFDSYTSYNQKFKGTTLTVDTSSS-----SAYMLLSSLTSEDSAVYFC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SFLT-----KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LELVATATGVNSQVQLQQPGAEIVRPGASVKLSCKTS-GYTFTDYW--MNWVKQRPGQGL
                                                                                                                                                                                                                                                                                                                                 HEALPMNFTOKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- ARGPRDSSGYYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGC
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Rodentia;
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                                                                                                                     Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 298.5; DB 1
Pred. No. 1.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4EEB5C253038B718 CRC64;
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                                                                                                                     update)
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Q80ZI7
         DRICK RACE OCCUPANT OF THE RESERVE OCCUPANT OCCU
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Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMB Submitted; (DEC-2001) to the EMB EMBL; BC019425; AAH19425.1; -.
MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 14; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 484 AA; 52859 MW;
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (MAR-2003) to the
EMBL; BC049143; AAH49143.1;
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                            Q80ZI7; PRELIMINARY;
Q80ZI7; TremBirel. 24,
01-JUN-2003 (TremBirel. 24,
01-JUN-2003 (TremBirel. 25,
01-OCT-2003 (TremBirel. 25,
                                                                                                                                                         Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Bukaryota; Metazoa; Chordatia;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARAYSNYYFDNWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTANSDTHLLQ-GOSLTLTLESPPGSSPSV-----QCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGRFTI-----SRDNSQNILYLQMN-----TLRAEDSATYYC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TCPELLGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%; Score 297.5; DB 11; ilarity 26.1%; Pred. No. 2.3e-16; Conservative 56; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGGKTLSVSQL---ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH---
                                                                                           N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431
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                                                                                                                                                                                                                                                                                 Last sequence up
                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
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Best Local Similarity 24.7
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00409; IGcl; 3.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 53019 MW;
                                                                                                                                                                                                                                                                                      Q96KX8
Q96KX8;
O1-DEC-2001 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
O1-OCT-2003 (TrEMBLrel.
Hypothetical protein.
Hymo sapiens (Human).
Eukaryota; Metazoa; Cho
                    Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC016369; AAH16369.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003906; Ig MC.
InterPro; IPR003906; Ig_v.
Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                            TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376
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     SM00406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDVWGAGTTVTVSSEPAREPTIYELTFPQALSSDPVIIGCLIHDYFPSGTWNVTWGKSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLLQGQSLTLTLESPPGSSPSV----QCRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVQPGGSMKLSCAAS-GFTFSNYWMNWVRQSPEKGLEWVAEIRLRSN--NYATHYAESVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKKGDTVELTCTASQKKSIQFHWKN-----SNQIKILGNQGSFLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIAKVTVNTFPPOVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPELLGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHEDPE-VKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRFTIS-RDDSKSSVYLQMN-----NLRAEDTGIYYCTRR------GYGDPNWY
                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTG
ig; 4; ; iGv;
                                                                                                                                                                                                                                                                                           Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%;
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, Last sequence up
, Last annotation :
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Pred. No. 2.
                                                                                                                                                                                                                                                                                           Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
i; Hominidae; Homo.
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[nterPro; InterPro;

IPR003599; IPR007110; IPR003597;

Ig. Ig-like. Ig_cl. Ig_MHC.

Nagahari S., Sasal

Sasaki Sugiyama ' Z.

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                                                                                                 TISSUE-Mammary gland;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T.,
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y.,
Suzuki Y., Nagai K., Sugano S., Ishii S., Kojima S., Nagah
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagah
Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., S
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AK074551; BAC11114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein FLJ90170.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBNCL6, PRELIMINARY; PRT; 493 AA.
QBNCL6, QNCL6,
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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IG_MHC; 1
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local Similarity
Matches 125; Conserv
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Q91WR1;

Q91WR1;

01-DEC-2001 (TrEMBLrel.

01-DEC-2001 (TrEMBLrel.

01-OCT-2003 (TrEMBLrel.

Hypothetical protein.

IGH-VJ558 OR AI893585.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 1.
SEQUENCE FROM N.A.
TISSUE-Kidney;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC01353; AAH13539.1; -.
MGD; MGI:96486; BP-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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SEQUENCE 493 AA; 53224 MW;
                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLLQGQSLTLTLESP------PGSSPSVQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRLTVS-RDNYKNTLY-----LEMKSLGAEDTAVYYC-ARDO----GYAGYGVF----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVVMAEVDGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TARNEPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQ----DVTVPCPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RSPRGKNIQGGKTLSVSQLELQDS-----GTWTCTVLQNQKKVEFKIDI-VPCPAPE
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1 (TrEMBLrel. 19,
3 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                     Chordata;
Rodentia;
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25.4%; Pred. No. 3.8e-16;
Live 67; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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Pfam; PP00047; ig; 4.
SWART; SW00406; IGv; 1.
SWOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
Hypothetical protein_
SEQUENCE 488 AA; 52964 MW; I
422
                           386
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                                                       EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDS
|||:||| :|| ||:||||:|| | ::| | ::| ||:
|PQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPG
                     DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
EGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                 KDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTF
                                                                                                                                                                         --- PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW----
                                                                                                                                                                                                                                                               LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH-----TCPELLGGPSV
                                                                                                                                                                                                                                                                                                                        TLESPPGSSPSV-----OCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                               LVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPY--NGGTSYNQKFKGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                            LGKKGDTVELTCTASQKKSIQFH--W---KNSNQIKILGNQGSFLTKGPSKLNDRADSRR
                                                                                                                                           KTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
                                                                                                                                                                                                     FLFPPKPK-----DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNA
                                                                                                                                                                                                                                  LASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGICSPPTT
                                                                                                                                                                                                                                                                                              TVSAEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPA
                                                                                                                                                                                                                                                                                                                                                     TLTVDKSSSIAYMQLNNLTSDDSAVYYC----ARGPVYYSYF----
                                                                                                                                                                                                                                                                                                                                                                                  SLWDQGNFPLI---IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $; Score 293; DB 11;$; Pred. No. 5.5e-16;73; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F12068460B400B9D CRC64;
                                                                                                                                                                                                                                                                                                                        -----PRG-KNI----QGGKTLSVSQL--E
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469
                             431
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RESULT 74 Q8N5K4 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR0073597; Ig-c1.
InterPro; IPR003597; Ig_wHC.
InterPro; IPR003596; Ig_w.
Pfam; PP00047; Ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00409; IGc1; 2.
SMART; SM00406; IGv; 1. Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chu
Mammalia; Eutheria; Pr Submitted (JUN-2002) to the EMBL; BC032249; AAH32249.1; Q8N5K4; 01-OCT-2002 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. Strausberg R.; SEQUENCE FROM NCBI_TaxID=9606; Q8N5K4 TISSUE=Blood; PS50835; PRELIMINARY; Z.A. Chordata; Primates; 22, Created)
Last sequence update)
Last annotation update) EMBL/GenBank/DDBJ databases Craniata; Vertebrata; Catarrhini; Hominidae; 499 ₹ Euteleostomi;

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PRESULT OF THE PRESUL
TISSUE-Gastric mucosa;

RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,

RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

RA Suzuki Y., Hata H., Nakagawa K., Mizuno S.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,

RA Kawakami B., Nagai K., Isogai T., Sugano S.;

"NEDO human cDNA seguencing project.";

RI Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

BR InterPro; IPR00316; Ig.MHC.

DR InterPro; IPR00316; Ig.MHC.

DR InterPro; IPR003596; Ig.MHC.

DR InterPro; IPR003596; Ig.MHC.
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Best Local S
Matches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96DKO PRELIMINARY; PRT; 496 AA.
Q96DKO;
Q96DKO;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 25, Last sequence upda
O1-OCT-2003 (TrEMBLrel. 25, Last annotation up
Hypothetical protein FLJ25298.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Primates; Catarrhini; Homi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSOO
Hypothetical
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APEPKSCDKTHTCPELLGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-----VWGKGTTVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVKGRFTIS-RDNAKNSLYLOMN-----SLRVEDTALYYCARDPTKYCSGGSCLGYYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGVV--RPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSS----INWNGGSTNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNKVVLGKKGDTVELTCTAS-------QKKSIQFHWKNSNQIKILGNQGSF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWTPSSGK--SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%;
26.1%;
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Pred. No. le-19
65; Mismatches
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Best Local
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PROSITE; PSS0835; IG MHC; 1.
Hypothetical protein.
SEQUENCE 496 AA; 53532 Max
                                                                                                                                                                                                                   Q9DCD9 PRELIMINARY; PRT; 425 AA.
Q9DCD9;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation updat Adult male kidney cDNA, RIKEN full-length enriche clone:0610041A01, full insert sequence.
Mus musculus (Mouse).
Mus musculus (Mouse).
            MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush
Schriml L. M., Staubli F., Suzuki R., Tomica M., Wagner L., Washio
                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     434
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LDETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LODSG-----TWTCTVLQNQKKVEFKI-----DI-VPCPAPEPKSCDKT
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                                                                                                                                                                                                       Rodentia;
                                                                                                                                                                                                                  Chordata;
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                                                                                                                                                                                                   Craniata; Veri
Sciurognathi;
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                                                                                                                                                                                                                     Vertebrata;
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enriched
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                                                                                                                                                                                                      Euteleostomi; 
; Murinae; Mus.
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Best Local S
Matches 106
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InterPro; IPR00357; Ig_Cl.
InterPro; IPR003506; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IGCl; 2.
SMART; SM00407; IGCl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 426 AA; 45819 MW;
                                                                                      Q91WP5
Q91WP5
Q91WP5
01-DEC-2001 (TrEMBLre1.
01-DEC-2001 (TrEMBLre1.
01-DCT-2003 (TrEMBLre1.
01-OCT-2003 (TrEMBLre1.
Hypothetical protein.
Mus musculus (Mouse)
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sabo K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AK002875; BAB22422.1; -.
PIR; F33932; F33932.
HSSP; P01810; 2FBJ.
Strausberg R.;
Submitted (SEP-2001)
                      SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                    NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                     LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLT
                                                                                                                                                                                                                                                                                                      GCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKNIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP-----PGS
                                                                                                                                                                                                                               VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                          LALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLR
                                                                                                                                                                                                                                                                                                                                                 SLORPALED-LLLGSDASLTCTLNGLRNPEGAV-FTW----EPSTGKDAVQKKAVQNSC
                                                                                                                                                                                                                                                                                                                                                                                              PAVECPEGESVKCSVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH-----PSL
                                                                                                                                                                                                                                                                                                                                                                                                                    ---ELQDSGTWTCTVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                         LPRALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSSLTSEDSAVYFCARSDYYGPYAMDYWG------QGTSVTVSSESARNPTIYPLT
                                                                                                                                                                                                                VSAELWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                           --YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                      FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST-
                                                                                                             (TrEMBLrel.
                                                                                                                      (TrEMBLrel.
                                                                                                                                 (TrEMBLrel.
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                  Chordata;
Rodentia;
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26.8%;
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Last annotation update)
                                                                                                                                 Created)
 EMBL/GenBank/DDBJ databases
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3; Mismatches
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Pred. No. 1.0
                                                                Craniata; Vert
Sciurognathi;
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                                                                  Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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Query Match
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SMART; SM00406; IGY; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
416
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TTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                  VQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQ
                                                                                                                                                                                                   -----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW-----EPSTGKDA
                        -SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                               VHLIPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGA
                                                                                 VYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG-
                                                                                                                                                                                                                                     PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                      QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCP----APEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                                                                                           LQMSSLRSEDTAFYYCVRGGYFDVWGAGTAVTVSSEPAREPTIYPLTFPQALSSDPVIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIKNLKIEDSDTYIC------EVEDQKE-EVQLLVFGLTANSDTHLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSPEKRLEWVAAINSNG----GNTYYSDTMKGRFTI-----SRDNAKSTLY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRGVPFRHILLVLQLALLPAATQ----GNKVVLGKKGDTVELTCTAS-------
                                                                                                                                                                  PREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                      CLIHDYFPSGTMNVTWGKSGKDIT-TVNFPPALASGGRYTMSSQLTLPAVEC--PEGESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QKKSIQFHWK---NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFP
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80
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Pred. No. 1.
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460
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Q7TMK4 Q7TMK4; Q7TMK4; 01-OCT-2003 (TrEMBLrel. 2 01-OCT-2003 (TrEMBLrel. 2 01-OCT-2003 (TrEMBLrel. 2 SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler

Klausmer R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F. Bukaryota; Metazoa;
Mammalia; Eutheria; Hypothetical protein. Mus musculus (Mouse). NCBI_TaxID=10090; Chordata; Rodentia; 25, Created) Last annotation Craniata; Vertebrata; Sciurognathi; Muridae; sequence 479 ₹ update) update) Euteleostomi; ; Murinae; Mus

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RESULT
OBVCV5
ID Q8VCV5
ID Q8
AC Q8
AC Q8
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Matches 117
                                                                     Q8VCV5
Q8VCV5;
Q1-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
Mus musculus (Mouse)
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                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN=C57BL/6J; TISSUE=Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; "Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                          NNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                              EKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCSGPTPPPPTTIPSCQ-----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGKN-----IQGGKTLSVSQL----ELQDSGTWTCTVLQNQKKVEFKIDIV
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Pred. No. 2.0
                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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PROSITE; PS0835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52326 MW;
                                                                                                                                                                                                                                                                                                                                                                        Q8WY24;
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF283666; AAL36697.1;
InterPro; IPR007110; Ig-like.
                                                                                                                Zheng
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01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                           Zheng S., Shao X., Cao J., Geng L., I
"Identification and characterization
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNTFP
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Pred. No. 2.8e
67; Mismatches
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Best Local Simi
Matches 129;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW; !
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Q9UP60,
01-MAY-2000 (Tr
01-MAY-2000 (Tr
01-OCT-2003 (Tr
SNC73 protein.
                                                                   SEQUENCE FROM N.A.

Zheng S., Cao J., Cao W., Cai X., Geng L.;

Zheng S., Cao J., Cao W., Cai X., Geng L.;

"Identification and characterization of SNC73,

regulated in colorectal cancer.";

submitted (JUN-1999) to the EMBL/GenBank/DDBJ

EMBL; AF067420; AAC19365.1;

HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
InterPro; IPR007110; Ig-like
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
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Primates;
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Last sequence up
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Pred. No. 3.2e-15;
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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ion of SNC73,
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                                                                                           InterPro; iPR007110; Ig-like.

InterPro; iPR003006; Ig_MHC.

InterPro; iPR003556; Ig_v.

R Pfam; PF00047; ig; 4.

R SMART; SM00406; IGv; 1.

R PROSITE; PS050835; IG_LIKE; 4.

PROSITE; PS050835; IG_LIKE; 4.

PROSITE; PS050835; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 479 AA; 51007 ...
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Best Local S
Matches 107
                                           Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                     EMBL; BC002091; AAH02091.1;
HSSP; P01810; 2FBJ.
InterPro
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00259; IG_MIC; 1.
SEQUENCE 384 AA; 40947 MW;
                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia;
                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99M22
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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107; Conserv
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HLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS-QKKSIQFHWKNSNQIKILGNQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDQGN-----FPLIKNLKIEDSDTYICEVEDQKEEVQLLVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAEPWNHCKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARNEPPSQDASGDLYTTSSQ---LTL-----PATQCLA--GKSV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
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llarity 23.2%;
Conservative 8:
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Last annotation update)
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                                          Score 281; DB 11;
Pred. No. 5.4e-15;
2; Mismatches 184
                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                      768E39A138918892
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                                                                                                                                                                                                                                                                                                                                      Murinae;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q29028 PRELIMINARY;
Q29028;
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_IKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    miniature. ";
J. Immunol. 151:1365-1370(1993).
EMBL, X65630; CAA46584.1;
PIR; 147132; S21462.
HSSP; P01730; 1CDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93329116; PubMed=8335933; Gustafsson K., Germana S., Sundt T.M., Extensive allelic polymorphion in an extensive allelic polymorphion in an extensive allelic polymorphion in an extensive allelic polymorphion in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=#1183; TISSUE=Blood;
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01-OCT-2003 (TrEMBLrel. 2
CD4, allele 2 (Fragment).
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9 AA;
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Last annotation updat
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                                                                                                               Score 280.5;
Pred. No. 6.8
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Mismatches 23
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  RESULT 85
Q8K0Z4
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AC Q8K0Z
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  Q8K0Z4
Q8K0Z4;
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Matches 104;
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Best Local Similarity
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HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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01-JUN-2001
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                        VFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWDQGN------PPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF-----GL 125
                                                                                                         CLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGN 406
                                                                                                                                               GCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLT
                                                                                                                                                                                  VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLT
                                                                                                                                                                                                                      ED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLS
                                                                                                                                                                                                                                                 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                                                                                                                                                                                                                                                                QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKP
                                                                                                                                                                                                                                                                                                                                                                      TARNFPPSQDASGDLYTTSSQ---LTL-----PATQCLA--GKSV
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                                                                    CLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGD
                                                                                                                                                                                                                                                                                             ----TCHVKHYTNPSQ----DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPAL
                                                                                                                                                                                                                                                                                                                                                                                                      T-----ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
TFSCMVGHEALPLAFTQETIDRLAGKPTHVNVSVVMAEVDGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 273.5; DB 4
Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OA9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500
                                  ----LQLDETC 438
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 499
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                                                                                                                                                                                    351
                                                                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                             281
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                                                                        456
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PRELIMINARY;

PRT;

480

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RESULT
Q90WB5
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
OS An
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Best Local S
Matches 116
Q90WB5
Q90WB5;
Q90WB5;
O1-DEC-2001 (TrEMBLrel. 19, Cr
O1-DEC-2001 (TrEMBLrel. 25, La
O1-OCT-2003 (TrEMBLrel. 25, La
T-cell surface glycoprotein CD
T-cell surface glycoprotein Cd
Anas platyrhynchos (Domestic d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR007101; Ig-21.
InterPro; IPR003597; Ig-AC.
InterPro; IPR003596; Ig-MC.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; Ig: 4.
SWART; SW00409; IG: 3.
SWART; SW00400; IGC1; 3.
SWART; SW00406; IGC1; 3.
SWART; SW00406; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MIC; 2.
SEQUENCE 480 AA; 51645 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R. Submitted (MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC029188;
                                                                                                                       86
                                                                                                                                                                    413
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                                                                                                                                                                                                                                                             329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               il Similarity 24.
                                                                                                                                                                 GEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                          REPOVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                     TIPSCQ----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGQSLTLTLES-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKATLTADKSSNTAYMHLSSLTSENSAVYFC------ARSKLGGFAYWG
                                                                                                                                                                                               SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                             FPPQVHLLPPPSEELALNELLSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEP
                                                                                                                                                                                                                                                                                           GKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNT
                                                                                                                                                                                                                                                                                                                       AKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                   KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                  NFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-VNCSGPTPPPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGTLVTVSAESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRRSLW---DOGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSD----THLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVKPGALVKISCKASGYTFTSFDISW-----MKQRPGQGPEWIGWISPGDGSSEYNEKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG----SFLT--KGPSKLNDRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAY-2002) to the EMBL/GenBank/DDBJ databases 19188; AAH29188.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.2%; bcc.
24.7%; Pre
24.7% 71;
 Last sequence update)
Last annotation update)
CD4 precursor.
c duck).
                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 270; DB 11; Length 480;
Pred. No. 4.5e-14;
1; Mismatches 178; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8690A63C669CDBED CRC64;
                                                                                          482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSVQCRSPRGKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                    461
                                                                                                                                                                                                 431
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RESULT 87
Q90524
ID Q9052
AC Q9052
AC Q9052
AC NOVel
DT 01-NC
DT 01-OC
DE NOVel
OS Gingl
OC Elasm
OC Elasm
OC Elasm
CC E
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Best Local S
Matches 95
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                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Novel antigen receptor (Fragment).
Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondr Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
NCBI TaxID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90524
Q90524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
TISSUE=Spleen;
MEDLINE=95183140;
Greenberg A.S., Av
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SMART; SM00409; IG; 3
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                                                                                                                    SEQUENCE OF 1-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissuz=Spleen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATADG-ELRETKKRSQALLEIPEMKRDSTVEV----KIHKIQLKHSGEYTCQLLYNRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WYVDGVEVHNAKTKPR------EEQYNSTYRVVSVLTVLHQDWL-NGKEYKCKV--SNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLT-LESPPGSSPS----------------------------VQCRSPRGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVFVLLQLGL--THIMAHQQQIGVEGKEVILNC---KKHDKDVTWKYEYDAGSSAIIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMDGKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQSKTELVVMQVSANPPGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES-NGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAAVDSTVTLSWHLNFRKIGWKEFF-----TGQLNWQEGNAITYELLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQGGKTLSVSQLELQDSGTWTCTVLQN----QKKVEFKIDIVPCPAPEPKSCDKTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVVKLTISSNGYFLPGDDLELTVMHKSPKSQPRFSITLFNSHNSRVTPEVLQNETPQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILAGK---IFKGRAPMSDRSET-----NONSKHLKVSNLRISDAGTYICECGSDRNSISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWK-----NSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENNYKT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KYALKVKQLQPTDSGTWICNMHSDSPSINENISFNVKVL------GFEKTHLERM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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       0; PubMed=7877689;
Avila D., Hughes
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22.2%;
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                                                                                                                I N.A.
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EMBL/GenBank/DDBJ databases
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Pred. No. 2.
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              Ξ
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          Hughes
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.8e-07;
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          Α.,
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              McKinney
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Best Local S
Matches 65
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Q9D8W4;
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
01-OCT-2003 (TrEMBLrel 2
1810027001R1k protein.
1810027001R1K
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MEDLINE=21085660; PubMed=11217051;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenby Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Wasl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
NON_TER
SEQUENCE
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Submitted
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Nature 374:168-173(1995).
                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18680; AAB48352.1; -. HSSP; P01842; 7FAB.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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(DEC-1994) to the
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268 AA;
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Pred. No. 2.2e
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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.2e-07;
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S., Yamanaka T
     Quackenbush
r L., Washio
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SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS500290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 24792 MW;
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InterPro; IPR00306; IG_MHC.
Pfam; PP00047; Ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LKE; 1.
PROSITE; PS00239; IG_MHC; 1.
SEQUENCE 130 AA; I4253 MW;
                                                                                                                                                                                                                                                            InterPro; IPR003599;
InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
InterPro; IPR003596;
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Q8N355;
01-QCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC028090; AAH28090.1; PIR; S12441; S12441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1916426; 1810027001Rik.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK007622; BAB25142.1; -.
PIR; S22760; S22760.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002
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Similarity 36.5%;
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Ig-like.
Ig_c1.
Ig_MHC.
Ig_v.
                                                                     24792 MW;
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7.6%;
25.0%;
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Pred. No. 1.
Score 183.5; DB Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                     CC848CAEBA4A9D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438197975E766E54 CRC64;
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                   Length
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Best Local Similarity

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RESULT 91
Q7Z3Y4
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Q99M11
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Matches 58
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Q99M11;
01-JUN-2001 (TrEMBLrel.:
01-JUN-2001 (TrEMBLrel.:
01-OCT-2003 (TrEMBLrel.:
  Q7Z3Y4
Q7Z3Y4;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. Mus musculus (Mouse).
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SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC002129; AAH02129.1; -. HSSP; P01703; 7FAB.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                               264 --VDGVEVHNAKTKPR-----EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                                                                               213 THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                        IEKTISKAKGQPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-EN 374
                                                                                                                                                                                                                                                                                                             NMIYGDDLRPSGVSDRFSGSIDSSSNSAF----LTIQNVQADDEADYYCQSYSSGIRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APVLVVVDDSDRPSGIPERFSGSNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFG
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                                                                                                                                           GVETTOPSKONNNKYMASSYLTLTAKAWETHSSYSCOVTHE---GHTVEKSLS
                                                                                                                                                                                  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
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                                                                                                                                                                                                                                                                                                                                                                                         TGSCAQLV-----LTQPSSVST-SLGSTAKLPCKASTGNIGDSYV--NWYQQYMGRSPT
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(TremBirel. 17, Last seq
(TremBirel. 25, Last ann
  (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                            PRELIMINARY;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 183.5; DB Pred. No. 3e-07;
                                          PRT;
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                                        RESULT 92
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Matches 75
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WEDLINE-22388257; PubMed-12477932;

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Toshiyuki S., Carainici P., Prange C.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Usdin T.B., Toshiyuki S., Carainici P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carainici P., Prange C.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S. J. Marra M. A.
Q8NFP4
Q8NFP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2001) to the EMBL; BC005332; AAH05332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
Homo sapiens (Human)
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01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                        212
                                                                                                                                                                                                                                                                                                                              184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
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                                                                                                                                                                                                                                                                                                                                                                                                            GLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF 123
                                                                                                                        KVYACEVTHQGLSSPVTKSFNRGE
                                                                                                                                                            KEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                       VVCLLNNFYPR--EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH
                                                                                                                                                                                                                                                                                                                              CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APKSLIYGASSLQSGVQSKFSGSGSGTDFTLTISSLQPEDFATYYCQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGLLLLCFPGARCDIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKP----GK
                                                                                                                                                                                                                                             VTCVVVDVSHEDPEVKFNWYVDGV--EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
                                                                                                                                                                                                                                                                                     ------KLEIK------RTVAAPSVFIFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25702 MW; 7FBFE4ED23084BC6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182;
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 107;
                   955
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Best Local S
Matches 99
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Genew; HGNC:19267; MDGA1.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016163; F:nitrogenase activity; II
GO; GO:0003399; P:nitrogen fixation; IEA.
InterPro; IPR003597; FN_III-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR003598; Ig-like.
InterPro; IPR000398; MAM_domain.
InterPro; IPR000398; MAM_domain.
InterPro; IPR000318; Nitrognse_compl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 6.
Pfam; PF000629; MAM; 1.
Pfam; PF000629; MAMDOMAIN.
SMART; SW00409; IG; 6.
SMART; SW00409; IGc2; 6.
SMART; SW00137; MAM; 1.
PROSITE; PS50085; IG LIKE; 6.
PROSITE; PS50060; MAM; 2; 1.
PROSITE; PS500699; NITROGENASE 1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Juan C., Iniesta P., Gonzalez-Quevedo R., Sanchez-Pernaute A., Torres A.J., Balibrea J. Cruces J., Benito M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed in human tissues and tumors."; Oncogene 21:3089-3094(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                          LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
                                                      SDYGTYLCMASFPGAPVPDLSVEVNIS----SETVPPTISVPKGRAVVTVREGSPAELQC
                                                                                                              GQDLKLSCHVDAVPQE--KVTYQWFKNGKPARMSKRLLVTRNDPELPAVTSSLELIDLHF
                                                                                                                                        SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                      AKKTVNLLVRSMKNATFQI - ·
                                                                                                                                                                                                                            TVQCLLTGGDPLPQLQWSHGPGPLPLGALAQGG
                                                                                                                                                                                                                                                       SVQC------RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN----
                                                                                                                                                                                                                                                                                   KLKNILRPODYASYTCOVSVRNVCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV
                                                                                                                                                                                                                                                                                                             - IKNLKIEDSDTYICEVEDQKE---EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP
                                                                                                                                                                                                                                                                                                                                           TVFLRCTVNSNPPARFIWKRGSD------TLSHSQDNG-VDIYEPLYTQGETKVL
                                                                                                                                                                                                                                                                                                                                                                    TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI
                                                                                  LNGKEYKCKVSNKALPAP---IEKTISKAKGQPREPQVYTLPPSRDELTKNQVS---LTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        955 AA; 105790 MW; BD41A1EB10A05962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin
                                                                                                                                                                                             QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                                                                                             7.5%;
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                                                                                                                                                                      ----TPDVI-----
                                                                                                                                                                                                                           -TLSIPSVQARDSGYYNCTATNNVGNP
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SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
SEQUENCE 379 AA; 42409 M
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01-OCT 2003 (TrEMBLrel. 25, Last and
Weakly similar to signal-regulatory
9930027N05RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANYOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome t
60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8BLX5;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Aorta, and MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8BLX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2444824; 9930027N05Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEVED 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPHCVLLLILLGLKGAAVRELKVIQPVKSFFVGAGGSATLNCTVTYLLPVGPIKWYRGV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPFRHLLLVLQLALLPAATQGNKVVLGKK-----GDTVELTCTASQKKSI----QFHWK
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FSCSVMH----EALHNH
                                                                                                   VSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                                                                                       LHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPS-----RDELTKNQ
                                                                                                                                                                                                                                                                                                                DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                    LELODSGTWTCTVLONOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK
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                                                                                                                                                      VLEPRDVRSQIIČEVDHVTLDRAPL---
                                                   INVTCQIQKFYPRRFQVTWLENGNISRREVPFTHIVNKDGTYNWISWLLVNISALEENMV
                                                                                                                                                                                                                                                          -------QNLTLKWFKNGNEISHLETSVEPEETSVSYRVSSTVQV
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                   -QQTVTFTC-----FFP----
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Pred. No. 9.3e-07;
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protein beta-1
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based o
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                                                                                                                                                      RGIAHISEIIQVPPTLEISQQPTMVWNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO07110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv; 1.
PROSTTE; PS50835; IG LIKE; 3.
SEQUENCE 397 AA; 44157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8BFX8
Q8BFX8;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK036935; BAC29645.1; -
EMBL; AK036935; BAC35818.1; -
EMBL; AK036945; BAC35818.1; -
EMBL; AK036445; BAC35818.1; -
EMBL; AK054945; BAC35818.1; -
EMBL; AK05494824; 9930027NO5Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary, and
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to signal-regulatory protein beta-1 precursor.
9930027NOSRIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                          FSCSVMH----EALHNH
                                                                                                 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                                         LHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPS-----RDELTKNQ
                                                                                                                                                                                                        ---QQTVTFTC----
                                                                                                                                                                                                                                                                         LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK
                                                                                                                                                                                                                                                                                                        QRG-----SSEPDIEIQSGGGTELSVFAKP-SSPMVS--GPAARAVP------
                                                                                                                                                                                                                                                                                                                                                                GOSRLLIYPFTGEYF----PRITSVSDVKKRSNLD---FSIRISNVTPADSGTYYC-VKF 121
                                                                                                                                                                                                                                                                                                                                                                                           NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEVED
                                                                                                                                                                                                                                                                                                                                                                                                                          IPHCVLLLILLIGLKGAAVRELKVIQPVKSFFVGAGGSATLNCTVTYLLPVGPIKWYRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPFRHLLLVLQLALLPAATQGNKVVLGKK-----GDTVELTCTASQKKSI----QFHWK
             VTCQVEHDGQAEVIETH
                                                                                                                            VLEPRDVRSQIICEVDHVTLDRAPL-----RGIAHISEIIQVPPTLEISQQPTMVWNV
                                                                                                                                                                                                                                                                                                                                   QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQ
                                                                       INVTCQIQKFYPRRFQVTWLENGNISRREVPFTHIVNKDGTYNWISWLLVNISALEENMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTCQVEHDGQAEVIETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                       -----SVEPEETSVSYRVSSTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 181; DB 1
20.1%; Pred. No. 1e-06;
Vative 70; Mismatches 1
                                          420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E1DE9DFAAC83D676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vagina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
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Best Local Similarity
Matches 124; Conserva
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 573 AA; 62967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8WU38
Q8WU38;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2002) to the EMBL; BC021276; AAH21276.1; PIR; S21205; S21205. Interpro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Tonsil;
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SRTILN--ASRSIEVS-YLAMTPLIPQSKDENSDDYTTFDDVGSLWTT 549
                         --ALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                      ALYYCAKHGSGSYI-----GYYYGMD----WGQGTTVTVSSAPTKAPDVFPIISGCRHPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAPGKGLEWVSGISWNSGSIGYADSVKGRFTIS-RDNAKNSLYLQMN-----
                                                                                SDIAVEWESNGQPENN---YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE- 415
                                                                                                                                                                                                                               EEKKKEKEEQEERETKTPECPSHTQPLGVYLLTPAVQD-LWLRDKATFTCFVVGSDLK
                                                                                                                                                                                                                                                         ------DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                       GEYKCVVQHTASKSKKEIFRWPESPKAQASSVPTAQPQAEGSLAKATTAPATTRNTGRGG
                                                                                                                                                                                                                                                                                                                    GTWTCTVLQNQKKVEFKI------DIVPCPAPEPKSC--------
                                                                                                                                                                                                                                                                                                                                                 DNSPVVLACLITGYHPTSVTVTWYMGTQSQPQRTFPEIQRRDSYYMTSSQLSTPLQQWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       DTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNQIK-----ILGNQGSF----LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MELGLSWIFILAILKGVQCEVQLVESGGGLV---QPGRSLRLSCAASGFTFDDYAMHWVR
                                                                                                              PPQRLMALREPAAQAPVKLSLNLLASSDPPEAASW-------LLCEVSGFSP
                                                                                                                                                                        DAHL--TWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNAGTSVTCTLNHPSL
                                                                                                                                                                                                   DPEVKFNWYVDG-VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                          ----APIEKTIS-KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62967 MW;
                                                                                                                                                                                                                                                                                                                                                                              IQGGKTLSVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 179.5; DB 4
21.1%; Pred. No. 2.2e-06;
Live 68; Mismatches 221
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FD072344033AC530 CRC64;
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                         -GLWTT 452
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; Homo.
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104 57

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Gaps

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RESULT 97
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Best Local Similarity
Matches 50; Conserv
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PIR; $12440; $12440.

GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:TRNA ligase activity; IEA.
GO; GO:0006418; F:TRNA ligase activation; IE.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003506; Ig_V.
InterPro; IPR001412; tRNA-synt_I.

Pfam; PF00047; 19; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS00179; AA_TRNA_LIGASE_I; 1.

PROSITE; PS00290; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96169;
Q96169;
Q1-DEC-2001
                                                                                                                                                                                                          Q90530 PRELIMINARY; PRT; 259 AA. Q90530; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-OCT-2003 (TrEMBLrel. 25, Last annotation Novel antigen receptor (Fragment).
                                                                     Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondr
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
NCBI_TaxID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                           SEQUENCE OF 1-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTISSVVAGDEADYFCQVWDTTSQQYVFGTGTQVTVLGQPKANPTVTLFPPSSEELQANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK--GQPR-EPQVYTLPPSRDELTKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTARITCGGSNLGSK----SVNWYQLRPGQAPILVVYENKERPAGIPERLSALTSEETAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTPEVTCVVVDVSHEDPEVKFNWY-----VDGVEVHNAKTKPR---EEQYNSTYRVVSV
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233 AA; 2
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                                 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24802 MW;
                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C694F8397B27650B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 1.1e-06;
Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEA.
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                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
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                                                                                                                                                             Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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RESULT
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Best Local
          "Increased Expression of VCAM-1 and ICAM-1 in Arteriopathy in the Dog."; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ EMBL; U32086; AAA84866.1; -. HSSP; P19320; 1VCA.
                                                                      Ballantyne C.M., Clubb F Youker K.A., Smith C.W., Willerson J.T.;
                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
Vascular cell adhesion molecule-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 2.

SMART; SM00407; IGC1; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greenberg A.S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95183140; PubMed=7877689; Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.; Plajnik M.F.; A new antigen receptor gene family that undergoes rearrangement
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       Q28260;
                                                                                                                                                                                                                                                   Q28260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U18687; AAB48358.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                         Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 374:168-173(1995).
                                                                                                                                   NCBI_TaxID=9615;
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                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         98
GO:0016020;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSVFLFPPKPKDTLMISRTPE------VTCVVVDVSH-----
                                                                                                                                                                                                                                                                                                                STS-----EIAVLLRDPTVEEIW
                                                                                                                                                                                                                                                                                                                                         SLSPGLQLDETCAEAQDGELDGLW
                                                                                                                                                                                                                                                                                                                                                                KNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQRKEIR
                                                                                                                                                                                                                                                                                                                                                                                        SNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                 YAACGAGTAVTVN--PGIPPSPPIVSLLHSATEEQRANRFVQLVCLISGYYPENIAVSWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISPGGRYVETVNSVQNLLINDLTVEDGGTYRCGGSL----YNW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEVKFNWYVDGV-EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   -APIEKTISKAKGOPREPOVYTL--PPSRDELTKNOVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:receptor
C:membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
28245 MW;
                                                                                                                                                   Carnivora;
                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TARVDQTPRSVTKETGESLTINCVLRDASYALGHTCWFRKKSGSTKEE
                                                                                   F.J., Perrard J.L.,
., Entman M.L., Hawk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity;
IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 176.5;
Pred. No. 1.3
                                                                                                                                                Craniata; Vertebrata; ; Fissipedia; Canidae;
                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                250
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                                                                                                                                                                                                                                                   739
                                                                                   J.L., Radovencovic Hawkins H.K., Fra:
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                                                                                                                                                                                                  update)
                                                           Early Cardiac
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                                                                                                                                                   Euteleostomi;
Canis.
                                                                                    Frazier
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                                                             Allograft
                                                                                     O.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CSCETDVLP
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Q6366
DG Q6466
DG VCAM-
GN VCA
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Best Local Similarity 21.5
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO03987; ICAM VCAM-1.
InterPro; IPRO07110; Ig-IIe.
InterPro; IPRO03598; Ig-C2.
InterPro; IPRO03598; VCAM-1.
Pfam; PP00047; Ig; 7.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM00408; IGC2; 4.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain.
SEQUENCE 739 AA; 81412 MW; BB51
                                                                                                                                                                                                                                                                                                  Q63669;
Q63669;
01-NOV-1996
01-NOV-1996
01-OCT-2003
SEQUENCE FROM N.A.
STRAIN-Sprague Dawley; TISSUE=Lung;
MEDLINE=92305064; PubMed=1377031;
Williams A.J., Atkins R.C., Fries J
Cybulsky M.I., Collins T.;
                                                                                                                                              Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                         VCAM-1.
                                                                                                                                                                                                                                                                             Vascular cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0016337; P:cell-cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVLTCGVTDCESPSFSWRTQIDSPLSGTVKVEGAKSTLTLSPVNLENEHSYLCTVTCGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEGGSVTMTCASEGLPPPQIFWSKKLDNGNLQLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECESKNEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS-DGSFFLYSKLTVDKSRWQQGNVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FL-----
                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
ll adhesion molecule 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNVPKTWII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 176.5; DB 6;
21.9%; Pred. No. 5.6e-06;
ative 65; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TIHKVQLEDAGVY
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                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GTOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB5DA3853739C615 CRC64;
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Q8N5F4;

PRELIMINARY;

PRT;

233

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01-OCT-2002 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.

22,

Created)
Last sequence update)
Last annotation updat

update)

Hypothetical protein. Homo sapiens (Human) Eukaryota, Merazoa, Chordata, Mammalia, Eutheria, Primates,

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A TISSUE=Brain, and Strausberg R.;

Lung;

NCBI_TaxID=9606;

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ID QRNSF4
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Best Local S
Matches 101
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PRINTS; PR01472; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00408; IGC2; 4.

PROSITE; PS50835; IG LIKE; 5.

Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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EMBL; X63722; CAA45254.1; -.

HSSP; P19300; IVCA.
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GO; GO:0016337; P:cell-cell adhes
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003989; VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 7.3%; Score 176.5; DB 1 Similarity 21.4%; Pred. No. 5.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGAAVTMTCASEGLPAPEIFWSKK------LDNGVLQLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EALHNHYTOKSLSL----SPGLQL-----DETCAEAQDGELDGLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPSDIAVEWE----SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHEDPEV-----KFNWYVDGVEVHNAKTKPREEQY----NSTYRVVSVLTVLHQDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA---GISKKSVELIIQGSSKDIQLTVFPSKSVKEGDTVIISCTCGSVPEIW
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25 739 VASCULAR CELL ADHESION MOLECULE 1.
739 AA; 81136 MW; A5AAD1172F67FB96 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PLSQNTTLSFMATKM-----EDSGIYVCEGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 131;
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Search completed: August Job time: 38.1743 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.2%; Score 174; DB 4; Length 233; Best Local Similarity 24.8%; Pred. No. 1.8e-06; Matches 55; Conservative 37; Mismatches 98; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                              178 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY----- 263
                                                                                                                                                                                                                                              374 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 CTVSEASYELTQPPSVSVSP------GQTARITC----SGDALPKKYAYWYQQKSGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TPYLVIYDDTERPSGIPERFSGSSSGTVATLTLSGAQVEDEADYYCYSSDSSGNHWVFGG 120
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Result
No.
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Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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21180.5
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                                     Beaudry GA, Maddon PJ;
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                                                                                                                                                                                                                                                                                                                                                                  1 chimeric heavy
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/note= "1. .25 =
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 435 AA;
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                                                                                                                                                                                                                                                                                                                                                 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKVIQGGKTLSVSQLELQDSGT
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                                                                                    FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                                 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
                                                                                                                                                                                                                 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
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                                                                   FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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97.7%;
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0; Mismatches
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RESULT 2
AAB3752
ID AAB3
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AC AAB3
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DT 27-A
DE Huma
XX
DE Huma

                                                                                                                                                                                                                                                                                                                                         Human; CD4; cluster of differentiation factor 4; immunoglobulin; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infect D2; alpha tailpiece; alphatp; fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE37574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE37574
                                                                                                                                                                                                           Homo sapiens
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                                                                             WO2003040311-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D1D2-Ig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alphatp fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (1g) comprising a hinge region and a constant domain of a mammalian Ig heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention are useful for preparing a composition for treating or preventing human immunodeficiency virus (HIV)-1 infection. The invention is useful in gene therapy and also in the preparation of vaccines. The present sequence is a fusion protein which comprises a human IgA alpha tailpiece (alphatp), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CD4 polypeptide ligated at its C-terminus with a portion of immunoglobulin, useful for preparing a composition for treating preventing HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 47; 100pp; English.
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DB; AAD29113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgG constant region comprising a hinge, a CH2 and CH3 region and CD4 D1D2 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                          ALHNHYTOKSLSLSPG------LQLDETC
                                                                                                        GFYPSDIAVEWESNGQPENNYKTTPFVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                                                                                                           QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
                                                                                                                                                                                                                                                                          LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVL-----ASADKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                              GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                                                                               QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
                                                                                                                                                                                                                                                  LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
ALHNHYTQKSLSLSAGKPTHVNVSVVMAEVDGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.7%;
93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2188.5; DB b;
Pred. No. 1.1e-115;
                                       438
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RESULT 3
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ID AAR2

AAR26531 standard;

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Matches 428
                                                                                                                                                                                                                             The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into M13mpl8. In order to excise a fragment containing the CH1 exon of the human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mpl8(CD4) vector. Oligonucleotide-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-IgGiHC-pRcCMV (ATCC 75192). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
28-JAN-1993
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 CD4-gamma 1 chimeric heavy chain homo-dimer and : for preventing and treating HIV infection useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-299758/36.
N-PSDB; AAQ27831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 4; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9213559-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of
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                        121
                                                                                                                                                       428;
121
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                                                                                                                                                                   Similarity
              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                         534
                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic agent;
LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 chimeric heavy chaim homodimer; expression vector; HIV;
diagnostic agent; inhibition.
                                                                                                                                                    90.1%;
nilarity 80.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4-IgG1 chimeric heavy chain heterotetramer
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(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CH1
303. .317
/label= hing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CH2
428. .534
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.427
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                                                                                                                                                    Score 2176; DB 2
Pred. No. 6.7e-11
0; Mismatches
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                                                                                                                                                                            Length 534;
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                                                                                                                                                                                                                                                                                                                                                                                                                  expression vector a diagnostic agent
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The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (Ig) comprising a hinge region and a constant domain of a mammalian Ig
                                                                                              Example 11; Page 67; 100pp; English.
                                                                                                                                              New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2001; 2001US-0346231P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2002; 2002WO-US034393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1; D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human FD1D2-Ig alphatp fusion protein variant
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DB; ACC82877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
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                                                                                                                                                         Fusion protein;
diagnosis; CD4;
                                                                                                                                                                                                     Genetic construct which encodes CD4 linked to human IgG1 at the upstream of the hinge region (fusion protein CD4E-gamma-1).
                                                                                                                                                                                                                                                      25-MAR-2003
02-NOV-1992
                                                                                                                                                                                                                                                                                                                                   AAP93009 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LHNHYTQKSLSLSPG------LQLDETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ 296
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milarity 92.5%;
Conservative
                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                       immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable
                                                                                                                                                                                                                                                                                                                                 protein;
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Pred. No. 1.4e-114;
3; Mismatches 11;
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22-JAN-1988; 20-JAN-1989;

88US-00147351 89EP-00100913

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Matches 427;
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Best Local
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(NO.67610). The plasmid containing (pCD4E-gamma-1) has been deposited in E. col1 (MC1061/P3) at the ATCC under accession number 67610. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin-CD4 fusion proteins - used for treating HIV infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-214472/30
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                               ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                             NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                             LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESSPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                       ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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67.8%;
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Pred. No. 4.9e-112;
0; Mismatches 4;
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MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

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RESULT 6
AAB19508
ID
AAB1
ID
AAB19508
ID
AAB1

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                            Query Match
Best Local :
  Matches 427;
                                                                                                                                                                                    The present sequence is that of fusion protein CD4Egammal comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge region (see AAA50661). Fusion protein CD4Egammal and a nucleic acid encoding it are claimed. Also claimed are vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Egammal provide both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
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                                                                                                                Sequence
                                                                                                                                                                and tissue stains. IgG1 fusion proteins such as CD4Egammal provide complement-mediated and cell-mediated immunity
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88.1%; ilarity 67.8%; Conservative
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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Pred. No. 4.9e-112;
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RESULT 7
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
WPI;
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Synthetic.
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anti-human immu
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immunodeficiency virus; CD4Egamma1.
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89US-00299596.
92US-00896781.
93US-00057952.
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RESULT 8
AAY59169
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AC AAY5
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AAY59169 AAY59169

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Best Local S
Matches 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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427; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
             WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                   ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                  ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                        NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                              LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                     QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Col 29-42; 39pp; English.
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Pred. No. 4.9e-112;
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Matches 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in animals, preferably humans treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Egamman where the CD4 is linked to human IgG1 at the Esp site upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion gene encoding immunoglobulin-CD4 fusion proteins, use the treatment of HIV or simian immunodeficiency virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-063015/06.
N-PSDB; AAZ48202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1989;
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protein; SIV infection; medicament.
                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        631 AA;
LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                             TWTCTVLQNQKKVEFKIDIV-----
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                                                          QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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Pred. No. 4.9e-112;
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25-MAR-2003
06-FEB-1993
was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses
                                                                                                     CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors treatment, prevention and diagnosis of HIV infection.
                                                                                                                                       WPI; 1992-300034/36.
N-PSDB; AAQ28088.
                                                         This sequence represents a CD4-gamma2 chimeric heavy chain homodimer.
                                                                                                                                                                        Beaudry GA,
                                                                                                                                                                                                                                                                   20-AUG-1992.
                                                                                                                                                                                                                                                                                        WO9213947-A1.
                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric;
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                                                                                                                                                                                               PROGENICS PHARM
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                                                                             Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                           increased serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     soluble CD4; T
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                                                                                                                                                                                                                     91US-00653684
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                                                                                                                                                                                                                                                                                                                         /label= CD4
217. .325
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326. .433
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                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          cell receptor; CD4 antigen; high recovery; half life; HIV infection; AIDS; ss.
                                                                                                    diagnosis
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RESULT 10
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ID AAR46
XX AAR46
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DT 05-M2
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XX CD4-9
XX CD4;
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                       Region
                                                                       Region
                                                                                                                       Region
                                                                                                                                                                          Region
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                               CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                            CD4-gamma 2
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08-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                            chimeric heavy chain.
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                                                                          /label= Hinge Region.
217. .325
                                                  label=
                                                                                                                                                  /label= CD4 Region.
                                                                                                                                                                                                  location/Qualifiers
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91.2%;
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Pred. No. 5.9e-112;
8; Mismatches 5;
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non- peptidy coxin or a gamma radiation-emilting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-I immuno:conjugates - used to kill HIV-infected cells and to stage HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432
               FSCSVMHEALHNHYTQKSLSLSPG
                                                                       VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                      VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
                                                                                                                                                                                             FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
                                                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIV-------PCPAPEPKSCDKTHTCPELLGGPSVFL
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                                                                                                                   VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
                                                                                                                                                                              FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV
                                                                                                                                                                                                                                       TWTCTVLONOKKVEFKIDIVVLAFERKCCVECPPCPAPP-
                                                                                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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 FSCSVMHEALHNHYTQKSLSLSPG
                                                         VSLTCLVKGF
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91.2%;
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Pred. No. 5.9e-112;
8; Mismatches 5;
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AAY85079
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KW CC91c
KW CC91c
KW CC91c
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AC C01c
AC CCC
                                                                                                                                                                                           This sequence represents the human CD4-gamma 2 chimeric heavy chain CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is CC linked to either the heavy chains or the light chains, or to all four C chains, directly or through a bifunctional chelator. Both heavy chains CC are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-CC [G2HC-pRcCMV (ATCC 75193) and both light chains encoded by vector CD4-CC chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-CC [G2HC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa CC (with the cell surface glycoprotein that is expressed on the surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and CC (MHC) class II molecules on the surface of antigen presenting cells to cells to cells. CD4 associates with major histocompatibility complex (munoconjugate is used to kil cells infected with HTV, and for treating CC (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used for imaging HTV-infected tissues (for staging and prognosis of HTV infected patients. The (complex of infection burden, once determined, this information is used in the staging and prognosis of HTV infected patients. The (complex of infection) are assembled intracellularly and secreted efficiently from mammalian (colls, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain (colls).
Query Match
Best Local S
Matches 405
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06-AUG-1993;
03-FEB-1995;
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                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY85079 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoconjugate, used to treat, prevent or image human immune iciency virus infection, comprises radionuclide attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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93WO-US007422.
95US-00379516.
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                            87.9%;
91.2%;
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Score 2122; DI
Pred. No. 5.9e
8; Mismatches
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   .9e-112;
шев 5;
                                                               DB 3;
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RESULT 12
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                                                                                                                             subject, co
comprising
kappalight
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-1992;
06-AUG-1993;
03-FEB-1995;
                                                                                                                               Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoconjugate; chelator; chimeric;
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                                                                                                                                                                                                                                                                                                                                                                    PROGENICS PHARM
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93WO-US007422.
95US-00379516.
95US-00477460.
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The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator.

Fig

3; 43pp; English

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AABBOORS ID AABBOORS AC AABBOORS HUMBAR AC AABBOORS HOME AC AABBOORS HOME AC AABBOORS AC A
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                                                                                                                            08-FEB-1991;
10-FEB-1992;
                                                                                                      08-DEC-1992;
                                                                                                                                                                                                                                                                13-FEB-2001
                                                                                                                                                                                                                                                                                                                 US6187748-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Anti-HIV; CD4-IgG2 chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CD4-gamma2 chimeric heavy chain homodimer.
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92WO-US001143.
92US-00960440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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91.2%;
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. No. 5.9e-112;
ismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                               heterotetramer;
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The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgG2HC-pRcCMV (V1) and CD4-kLC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4-cell by a HIV and to prevent CD4+ cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+ cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ or treating a subject having CD4+ cells infected with HIV involves CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
Sequence 432 AA;
                                                homodimer. This sequence was used in the method of the present invention
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DB; AAF77829.
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RESULT 14
ABG71122
ID ABG71
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AC ABG71
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Pred. No. 5.9e
8; Mismatches
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.9e-112;
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CD4-gamma2 17-JAN-2003

chimeric heavy

chain

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the CD4-IgG2 chimeric protein.

(first

entry)

ABG71122

standard;

protein;

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Query Match
Best Local Similarity
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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CI-1gG2HC-pRcCMV, and two light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (II) linked to a toxin, are useful for inhibiting HIV infection of a CD4-cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4; gamma2
mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 432 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes
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DB; ABS55720.
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                   FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP---
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91.2%;
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chimeric heterotetramer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a purified CD4-immunoglobulin (Ig)G2 chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immunodeficiency virus-1; HIV-1; mutant;
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Pred. No. 5.9e-112;
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This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer It was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block

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AAR26783

ID AAR26

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25-MAR-2003
06-FEB-1993
                                                                                                                                                                                                                                                                                          CD4-gamma-2 and CD4-IgG2 chimera(s)
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                                                                                                                                                                                                                                                                   prevention and diagnosis
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(revised)
(first entry)
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  07-AUG-1992;
06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                           CD4-IgG2 chimeric heavy chain heterot cytotoxic radionuclide; cell surface
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                                                                              07-JUN-1995;
                                                                                                                                                                                      US6034223-A.
                                                                                                                                                                                                                                                                                          prognosis; envelope
                                                                                                                                                                                                                                                                                                                        cellular
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                                                                                                                                                                                                                                                                                                                   c radionuclide; cell surface glycoprotein; immune response interaction mediator; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM
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  92US-00927931
93WO-US007422
                                                                                 95US-00477460
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                                                                                                                                                                                                                                                                                          glycoprotein
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77.3%;
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Pred. No. 9e-110;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                           heterotetramer; immunoconjugate; treatment; surface glycoprotein; prevent; infection;
                                                                                                                                                                                                                                                                                             burden; human
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Sequence

530 AA;

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CC sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a CC heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or to all four chains, directly or through a bifunctional chelator. Both CC to all four chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-KD2HC-pRCCMV (ATCC 75193) and both light chains are chimeric CD4-Ig (immunoglobulin) G2 chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-KLC-pRCCMV (ATCC 75194). CD4 is a CC non-polymorphic cell surface glycoprotein that is expressed on the Surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 associates with major histocompatibility complex CC (MHC) class II molecules on the surface of antigen presenting cells to mediate efficient cellular immune response interactions. In humans CD4 is che target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating cor preventing infection. It is also used for imaging HIV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used to determine the HIV convelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The convelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The staging of interaction is essembled intracellularly and secreted efficiently from mammalian colors, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain colling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoconjugate, used to treat, prevent or image human : deficiency virus infection, comprises radionuclide attached heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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δ 밁 Ş 밁 Ś á á 문 밁 문 δ Matches 409; Query Match Best Local : 181 181 121 301 241 121 61 13 \vdash Similarity MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG ILGNQGSFLTKGFSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP TWTCTVLQNQKKVEFKIDIV-----LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK Conservative 86.4%; Score 2085; DB 3 Pred. No. 9e-110; 9; Mismatches 1 13; u T PCPA---Length Indels 98; Gaps -PEP 207 180 180 120 120 60 300 240 207

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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotestramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                                                                                                                                                                                          Sequence 530
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10-FEB-1992;
08-DEC-1992;
The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has
                                                                                                                                                                                                                                  Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves usin CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
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DB; AAF77830.
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                         Protein
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"Mature CD4-IgG2 chimeric heterotetramer"
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Pred. No. 9e-110;
9; Mismatches 13;
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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD4-IGG2HC-pRcCMV, and two light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-immunoglobulin G2 chimeric heavy chain chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 530 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRCCMV and CD4-kLC-pRCCMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 4A-H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-038273/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABS55721.
                                                                                                                                                                                                                                                                                                                                                                          | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKYVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                           YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS
                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                       TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
                                                                                                                          ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                    VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK
                                                                                                                                                                                                                                 TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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92US-00960440
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Pred. No. 9e-110;
9; Mismatches 13;
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421

KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM

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Best Local S
Matches 419
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding amino acids 1-173 of cD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 59-70;
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N-PSDB; AAZ44065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human fusion protein CD4Bgammal
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                                                                            LVFGLTANSDTHLLQGQSLTLTLESSPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
TWTCTVLQNQKKVEFKIDIV---
                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                        MRGVPFRHLLUVQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQPHWKNSNQIK
                                                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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89US-00299596.
92US-00896781.
93US-00057952.
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68.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the treatment of human immunodeficiency virus.
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Pred. No. 1.8e.
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     DB 3;
1.8e-109;
1es 11;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 616;
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                                                                                                                                                                                                                                                                                          HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein; secreted protein; SIV infection; medicament.
                                                                                        New
                                                                                                           WPI; 2000-063015/06.
N-PSDB; AAZ48205.
                                                                                                                                         Seed
                                                                                                                                                                                                                                         CA1340741-C.
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                        CD4-Ig fusion
                                                                                                                                                                                                                                                                                                                                             14-MAR-2000
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                                                                                                                                                                               20-JAN-1989;
                                                                                                                                                                                                   20-JAN-1989;
                                                                                                                                                                                                                       14-SEP-1999
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP.
                                                                            fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in treatment of HTV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL
                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encode

Example 1; Page 61-68; 89pp; English

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AAP9308
ID AAP93
XX AAP93
XX AAP93
XX AAP93
XX AAP93
XX AAP93
XX 25-M2
DT 25-M2
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XX Genet
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Best Local :
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                                           Genetic construct which encodes CD4 linked to human IgG1 at the site upstream of the CH1 region (fusion protein CD4H-gamma-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Bgammal where the CD4 is linked to human IgG1 at the Banl site downstream from the hinge region
diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region
                 Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
                                                                                                                                      AAP93008;
                                                                                                                                                                AAP93008 standard; protein;
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. No. 1.8e-109;
ismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The fusion protein genes of the invention pref. comprise cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see WO87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4E-gamma1, and CD4Mmu (NO.67608), pCD4P-gamma (No.67608) and pCD4E-gamma. (No.67608) and pCD4E-gamma-1 (NO.67608) at the ATCC under accession number 67611. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Infections or detecting HIV or SIV in sample.
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                                                                                                                                                                                                                                                                                                                                                                1LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 1, Page 12-23; 68pp; English.
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                        LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG 420
                                                                                                               LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIV------
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Pred. No. 2.6e-109;
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
            The present sequence is that of fusion protein CD4Hgammal comprising textracellular portion of CD4, which binds to HIV gpl20, linked at its terminus to the human IgG1 heavy chain. To obtain the fusion protein, encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the region (see AAA50660). Pusion protein CD4Hgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucl
                                                                                                                                                                                                                                                                                                    CD4-immunoglobulin SIV.
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DB; AAA50660.
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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Best Local Sim
Matches 428;
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KSLSLSPG
                                                              VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                    VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                   VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                    ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                           LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                        TAALGCLVVSYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                                                                                   -----PAP-----
                                                                                                                                                                                                                                                                                                                                                         LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                             QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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58.8%;
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Pred. No. 2.6e
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2.6e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in animals, preferably humans they are also useful infections in humans. The present sequence represents the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion gene encoding immunoglobulin-CD4 fusion proteins, useful treatment of HIV or simian immunodeficiency virus infections.
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                           TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
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Pred. No. 2.6e
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es 3;
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08-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                        AAR46679;
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                                   Allaway GP,
                                                                           07-AUG-1992;
                                                                                               06-AUG-1993;
                                                                                                                  17-FEB-1994.
                                                                                                                                      WO9403191-A1.
                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                         CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatme
                                                                                                                                                                                                                                                                                               imaging;
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                                                        PROGENICS PHARM
                                                                                                                                                                                                                                                                                                                                       chimeric heavy chain.
                                                                                                                                                                                                                                                                                                detection; targetting;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
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N-PSDB; AAQ55751 WPI; 1994-065392/08.

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Fusion protein; human; CD4; IgG1; immunoglobulin; anti-human immunodeficiency virus; CD4H-1.
                                         Human fusion
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                                                                     23-MAR-2000
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                                                                                                                            standard;
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                                         protein CD4H-1
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4H-1 which is constructed from CD4 linked to human IgG1 upstream of the CH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                        LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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92US-00896781.
93US-00057952.
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D; Mismatches 4;
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virus

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                     The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see Wo87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The 19 heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4Hlambda1, CD4Fmu, CD4Elambda1, and CD4Mmu (No. 67608), pCD4Plambda (No. 67609) and pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
Sequence
                                                                                                                                                                           Example; Table 5, Page 48-55; 68pp; English.
                                                                                                                                                                                                   Immunoglobulin-CD4 fusion proteins - used for treating infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                           WPI; 1989-214472/30
                                                                                                                                                                                                                                                                                                                                            22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein; diagnosis; CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic construct which encodes CD4 linked to human IgG1 at the Ban1 downstream from the hinge region (fusion protein CD4Blambda1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
03-AUG-1992
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable region.
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Query

Match

85.2%;

Score

2056;

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                                                                                                                              gp120;
                                                                                                                                                                               09-JAN-2001
                                                                                                                                                                                                  AAB19511;
                                                                                                                                                                                                                     AAB19511 standard; protein;
           12-SEP-2000
                                                           Protein
                                                                                                                                       CD4; IgG1; human;
                                                                                                                                                           CD4-IgG1 fusion
                              US6117656-A
                                                                              Protein
                                                                                                          Homo sapiens
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                                                                                                                             therapy;
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                                                                                                                                                                                                                                                                                  LHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                            FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                                                                                                                                                                                                         FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
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                                                                                                                                                                                                                                                                       LHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                   DWLNGKEYKCKVSNKALPAPIEKTIS-
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                                                                                                                                                                               (first entry)
                                                                                                                              n; CD4Bgammal;
diagnosis.
                                                                                                                                                           protein CH4Bgammal.
                                                         /note=
                                                                           Location/Qualifiers
1. .395
                                                         .616
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                                                                    "CD4 extracellular
                                                "IgG1 heavy
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1; Mismatches 12;
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                                                                                                                                        fusion
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                                                 chain'
                                                                                                                                      protein; immunoglobulin;
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                                                                                                                                        HIV;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4-immunoglobulin fusion proteins, useful for targeting
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12-APR-1993;
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23-JAN-1989;
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                                                                                                                                                  LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                               MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                                                                                                                                             QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                        -----APEPK---
                                                                                                                                                                                                                                                                                                     TWTCTVLQNQKKVEFKIDIV------PCP----
                                                                                                                                                                                                                                                                                                                                  LVFCLTANSDTHLLQGQSLTLTLESPPCSSPSVQCRSPRCKNIQCCKTLSVSQLELQDSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
                            MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRYVSVLTVLHQ
                                                                                         LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL
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                                                                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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Pred. No. 7.
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ARESULT 29
AAW35860
ID AAW35860
AC AAW35
AC AAW3
                                                  CC A novel T lymphocyte veto molecule is a chimeric molecule comprising a CC protein, e.g. the present sequence, linked to a targetting polypeptide CC that binds a molecule, which differentiates a host cell from a tissue CC graft cell, or selectively targets a stimulator cell involved in the CC autoimmune response. A veto molecule, in which the protein binds a CC molecule that targets stimulator cells, can be used to suppress an immune CC response and therefore treat autoimmune diseases, e.g. systemic lupus CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune CC allergies and other immunological disorders. Where the protein binds a CC molecule that differentiates graft and host cells, the veto molecule can be used to reduce transplant rejection. The veto molecule provides specific regulation of particular stimulator cells that can kill graft CC cells or respond to autoantigens, but leave other stimulator cells can ceffected, e.g. CD4 or CD8 positive cells can be regulated without one minimise generalised immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tlymphocyte veto molecule comprising response cell activating protein linked to molecule that targets stimulator cell marker, used for selective suppression of immune response, e.g. prevention of graft rejection or treatment of auto-immune disease.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-512419/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
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   410
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Query Match

68.2%;

Score 1647.5;

DB 2;

Length 410;

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RESULT 30
AAR20634
TY YOU WANTE TO THE TENT OF YOUR WANTE WANTE TO THE WANTE WAS AND 
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                   N-PSDB;
                                                                                                                                                                                  11-JUL-1990;
05-MAR-1991;
                                                                                                                                                                                                                                                        11-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4; LTI; Streptomyces longisporous; HIV gp120; AIDS; IgG1; T cell; immunoglobulin; surface glycoprotein; virus; MHC class II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric protein V1V2-hCH2-KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR20634 standard;
                                                                                                                                      (SMIK)
                                         1992-056814/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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                                                                                          Σ
ΕΊ
                                                                                                                                      SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPDVQISWFVNNVEVHTAQTQTHREDYNSRLRVVSALPIQHQDWNSGKEFKCKVNNKDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGPTIKPCP---PCKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APIERTISKPKGSVRAPOVYVLPPP-EEMTKKOVTLTCMVTDFMPEDIYVEWTNNGKTEL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                       Fornwald JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                  90US-00551584.
91US-00665218.
                                                                                                                                                                                                                                                        90US-00551584
                                                                                                                                                                                                                                                                                                                                                                                                                                        214. .228
/label= hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 28. .29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29. .213
/label= V1V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= signal_cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                       Arthos J;
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1; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
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Nucleic acid sequences for production of CD4 chimeric protein - used to transfect streptomyces, contg. LTI signal sequence linked to pro-peptide sequence facilitating peptide cleavage.
```

English.

The sequence was deduced by sequencing the plasmid vector VIV2-hCH2- KA CC in S. lividans strain 1326. The protein has domains contg. peptides of CC different function. It contains a CD4 chimera (VIV2) in which the carboxy terminal portion of the protein consists of a murine immunoglobulin light CC chain constant region, linked to the signal peptide of Streptomyces LTI, CC modified at its N-terminus to include Lys-Arg. Also included is the IgG1 CC constant region comprising the hinge and CH2 metotifs. Human IgG1 is the CC complement and ADCC. The CD4 chimeric proteins may be expressed in CC complement and ADCC. The CD4 chimeric proteins may be expressed in CC complement, and the LTI CD4 protein increases the stability of the CD4, CC thus increasing the serum half life and/or potency against HIV infection CC and inhibit virus-induced cell fusion, relative to soluble CD4. By CC altering only one amino acid at position 2 near the N terminal of CD4 (VI region) from Lys to Ala, a heterologous protein is expressed which is cfficiently secreted and correctly processed to remove the entire LTI CC signal sequence, but which still retains the gp120 binding capacity. By condifying the pro-peptide you avoid deleterious effects of additional CC amino acids on the function of the protein. See also AAR20635,6

Sequence 343 AA;

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 Local
 322
                               309
                                                              262
                                                                                            249
                                                                                                                           202
                                                                                                                                                          199
                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                               300;
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                                                                                                                                                                                                                                                                                      79
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                     RADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS
                                                                                                                                                                                                                                                                                                                                      LPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND
                        SNKALPAPIEKTISKAKGQPRE 330
                                                                               VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                           IVVLAFQKASKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                            IV----PCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                    RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS
SNKALPAPIEKTISKAKGOPRE
                                                              VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                        LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                                                  LTGAALAKAVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                               64.0%;
93.2%;
                                                                                                                                                                                                                                                                                                                                                                               Score 1546; D. Pred. No. 1.5e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 0;
343
                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 343;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                321
                                                                                                                           261
                                                                                                                                                         248
                                                                                                                                                                                        201
                                                                                                                                                                                                                       198
                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                    138
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ARBSULT 31
AARB9441
ID AARB9
XX AARB9
XX AARB9
XX DT 26-SE
XX UT9G1
XX CD7;
KW CD7;
KW CD7;
KW dendi
XX CD7;
XX Homo
XX Homo

CH2

26-SEP-1996

(first and

entry) CH3 domains

AAR89441 standard; peptide;

254

8

dendritic cell;

CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;

therapy; mammal; infection

δ 밁 Ş 밁 S 밁 S 밁 Ş

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RESULT 32
AAR78667
ID AAR78
XX
AC AAR78
XX
DT 11-AF
XX
DE IGG1
XX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is included in the membrane bound protesinaceous chimeric receptor of the invention. Alternatively the transmembrane region of the chimeric receptor contains a portion of the CD7, CD5 or CD3 transmembrane domains. The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, neutrophils, or dendritic cells. The therapeutic cells expressing the chimeric receptor are administered to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mammal to treat HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.
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24-FEB-1995;
           IgG1 hinge,
                                         11-APR-1996
                                                                                               AAR78667 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human IgG1 hinge, CH2 and CH3 sequence is included in the membrane bound proteinaceous ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 25; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1995;
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DB; AAT10780.
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                                                                                                                                                                                                                                               PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGLQLDETCAE 440
                                                                                                                                                                                                                                                                                     ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                      I SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTP
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                                                                                                                                                                                                AQDGELDGLWTTDP 454
                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
                                                                                                                                                                    Conservative
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             CH2 and
                                         (first entry)
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95US-00394388
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                                                                                               protein; 254
             CH3 domains
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98.0%;
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RESULT 33
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01-JAN-2004 ADD13790;

(first entry

ADD13790 standard; protein; 400

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380

180

320

60

120

440 240

library; transfection; humanized monoclonal T cell receptor; circular.

antibody; antigen,

protein.

Plasmid pBS loxP-IgG1/pBS loxP-IgG1delta350/pBS loxPIgGdeltaCH1

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Matches 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Target cytolysis of HIV-infected cells.
                                                                                                                                                                                                                                                                                                                         Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis; buman immunodeficiency virus; adoptive immunotherapy; IgG1.
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                                                   PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                   AQDGELDGLWTTDP 454
                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAB
                                                                                                                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                 EPKSCOKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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AODGELDGLWTTDP
                                                                                                         ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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94US-00284391.
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                                                                                                                                                                                                                                                                    Score 1332.5; DB Pred. No. 1.2e-67; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by chimeric CD4 receptor-bearing
                                                                                                                                                                                                                                                                                              DB 2;
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Best Local S
Matches 266
                                                                                                                                                                                            monoclonal antibodies, for selection of those with affinity for particular antigens and useful for diagnostic or therapeutic use. Libraries of T cell receptors may also be prepared. The method produces libraries of high diversity; provides easy, quick and automatable selection from a large number of proteins, allows relatively simple alteration of the expressed gene (e.g. fusion to other protein-coding sequences), is suitable for large scale protein production and allows simple verification and characterization of selected cell lines. The method does not require incorporation of a resistance marker. This sequence represents the construct pBS loxP-1gG1/bBS loxP-1gG1delta350/pBS loxPIgGdeltaCH1 described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method of preparing a library of protein producing sukaryotic cells comprising (a) introducing specific recombination signals into one or two chromosomal gene loci, (b) Expanding at least one of the modified cells, (c) Transfecting many different DNA sequences, each flanked by recombination signals, into the expanded cells and (d) Integrating the DNA sequences into the gene loci on the basis of the recombination signals and the appropriate recombinase. The resulting cells express different proteins, each from an integrated DNA sequence and the proteins are bound to the cell surface. The method is particularly used to produce libraries of humanized monoclonal antibodies, for selection of those with affinity for
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Region
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                                                                                                                                                                   Sequence 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 19; Fig 16; 75pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparing library of protein-producing eukaryotic cells, useful producing humanized high-affinity antibodies, comprises introduc specific recombination signals into chromosomal gene loci and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breitling F, Moldenhauer G,
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Homo sapiens.
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                                                                                               Local Similarity
les 266; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variety of DNA sequences.
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                               PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
                                                                PSVQCRSPRGKNIQGG-----KTLSVS----
                                                                                                   Conservative
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/note= "Murine IgG1 M1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223. .329
/note=_"Human IgG1 CH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "human IgG1 CH2"
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                                                                                                               55.0%;
75.4%;
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-TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLG
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                                                                                                 Score 1327.5; DB 7;
Pred. No. 3.7e-67;
8; Mismatches 22;
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                                                                                                 Preparing library of protein-producing eukaryotic cells, useful for producing humanized high-affinity antibodies, comprises introducing specific recombination signals into chromosomal gene loci and integrating
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                                                                                                                                                                                                                                                                                Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001; 2001EP-00123596
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                                                                            variety of DNA sequences.
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Example 1; Fig 12B; 75pp; German

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Best Local Similarity
Matches 266; Conser
                                                                                                                                                                                                                      Antiinflammatory; antibacterial; immunosuppressive; antirheumatic; antiarthritic; immunomodulator; concatameric protein; soluble doma dimeric protein; inflammation; septicaemia; cytotoxicity; rheumatoid arthritis; cachexia; inflammation; human.
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7; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel concatameric protein comprising two soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New concatameric protein having two soluble domains, useful for diagnosing and treating disorders associated with the dimeric pits glycosylated form, such as inflammation, septicemia, rheumanthritis and cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein or its glycosylated form, such as inflammation, septicaemia, cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-related diseases. This sequence represents the human concatameric protein
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                                                                                                                                                                             DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                        SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                 FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                                                                                LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE
                                                                                                                                                                                                                                                                                                                                                                                          IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ------SLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                       DDIKWEKTSDKKKIAQFRKEKE-----TFKEKDTYKLFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han
ង្គ
                            PG 431
                                                        GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                   NKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                                CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
                                                                                                                                                                                                                                                                                                                                                          KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002WO-KR001427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1287.5;
Pred. No. 7.3e.
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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RESULT 36 AAR42162

AAR42162

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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                         BBV-transformed cell lines and mouse-human heterohybridomas producing human MAbs specific for the 9p120 V3 loop of HIV-1 MN isolate were obtained. MAb 447-52D was found to recognise the tetrapeptide motif GPGR, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the H chain V region was derived from 447-52D and to which a signal sequence and a H chain intronic sequence are appended, fused to a fragment contg. a short intronic sequent of the human gamma 1 crooding domain in its genomic form. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HIV-neutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune deficiency syndrome; chimeric antibody; surface glycoprotein gp120; V3 loop.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 2A; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant human antibody - wat least two isolates, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-336600/42.
N-PSDB; AAQ49834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09319785-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-HIV-1 recombinant antibody 447-52D heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR42162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC
                                                       210
                                                                                    180
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265
                            234
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                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                    GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS
                           CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                   CDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
                                                                                                               ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS
                                                                                                                                              VWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
                                                                                                                                                                       --- GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----
                                                                                                                                                                                                    TISRDDSKNTLYLOMN-----SLKTEDTAVYSCTTDG----FIMIRGVSEDYYYYYMD 119
                                                                                                                                                                                                                                 ---RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ 135
                                                                                                                                                                                                                                                              LVKPGGSLRLTCVASGFTFSDVWLNWVRQAPGKGLEWVGRIKSRTDGGTTDYAASVKGRF
                                                                                                                                                                                                                                                                                       LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conley
                                                                                                                                                                                                                                                                                                                      Conservative
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(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                   53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GE,
                                                                                                                                                                                                                                                                                                                      Score 1287; DB 2;
Pred. No. 8.2e-65;
0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with HIV new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV neutralising activity against venting or treating infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfarr
                                                                                                                                                                                                                                                                                                                                                  Length 461;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                         ---KTLSVS-----
                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                      264
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RESULT 37
AAO18400
ID AAO11
XX AAO1
XX AAO1
XX Matu
XX Mous
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                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to humanised anti-lymphotoxin beta recepton (LT-beta-R) antibodies. These are derived from the murine LT-beta-R binding antibody (CBE11 and can be used to treat neoplasia in humans. The present sequence is a humanised murine CBE11 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-lymphotoxin-beta receptor antibody, useful treating or reducing the advancement, severity or effects of particularly solid tumors (i.e. carcinomas) including colorect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2000; 2000US-0240285P
13-MAR-2001; 2001US-0275289P
21-JUN-2001; 2001US-0299987P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583337/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garber E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001; 2001WO-US032140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature humanised murine CBE11 heavy chain variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA018400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humanised antibody; lymphotoxin beta receptor;
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                      ISRDNAKUSLY-----LQMSSLRAEDTAVYYCAREE
                                                                                                                                                                                                                                                         LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFLTKGPSKLN----
                                                                                                                                                                                                                                                                                                                                                                                                                      449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
WGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                -GOSLITLILES PPGSS PS VQCRS PRGKNIQGG------KTLSVS-----
                                                                                                                                                     -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ-
                                                                                                                                                                                                           LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyne P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 25-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT-beta-R; light chain;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saldanha
                                                                                                                                                                                                                                                                                                                                     59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449
                                                                                                                                                                                                                                                                                                               Score 1285.5; DB 5;
Pred. No. 9.7e-65;
9; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; cancer;
                                                                                                      ----NGNFYYFDY 109
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                                                                                                                                                                                                                                                                                                                                                                     449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of neoplasia,
                                                                                                                                                                                                                                                                                                               91;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
  169
                                                   172
                                                                                                                                                          135
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